

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTCGTCTTCCG
CAGCGCTACCCGCCATGCGCCTGCCGCCGGCCGCTGGGGCTCCTGCCGCTTGCTG
CTGCTGCCGCCGCCGGAGGCCAAGAAGCCGACGCCCTGCCACCAGGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAAGAAACTTGGCGGCGGGAAACA
CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCGACTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGGAGATGGAGCAGACA
GGCGACGGGTCCGTGCCGCCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGGAACCGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCTGACCAACAGAGACTGCCGGAGTGTGAAGTGGCTGGTGCT
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCGAGCCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAAACCTGTGAGGAAAAACG
AAAAGTGTACAATACTCCAGGGAGCTACGTCTGTGTGCTGACGGCTTCGAAGAAACG
GAAGATGCCGTGTGCCGCCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGGAAGACCTGTAATGTGCCGGACTTACCCCTAAATTATTCAAGAAGGATGTCC
CGTGGAAAATGTGCCCTGAGGATGCCGTCTGCAGTGGACAGCGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCCTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATATTTGATACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAA^
TTGGCCGCCATGGCCCAACTGTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTCAAAATAAGCATTTCACACTGCATTCTAGTTGTGGTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGGATTAAATTGGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGGCGAAAGAACCAAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAAKKPTPCHRRCRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHTSICTACDESCKTCSGLTNRDCGECEVGWLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAC TGCACCTCGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACCGTCCGCCAGGCCGGAGGCACCGCCCAGCCGTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTCCCGCAGCGAGGAGGAGTCCTGAGCAGCAGCATGGCCGGAGGAGCGCCTTC
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC
CGGGCCGCCGCAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAAGGCAAGAGTACTCA
TAGGATTGAAGAAGATATCCTGATTGTTCAGAGGGAAAATGGCACCTTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCCGTCAATATCCATTCCATGAATTTC
CTGGCAAGCTGCAGGGCAGGCAGAATACCTCTATGAATTCTGCTGCCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGAACAGTGCCTCACAGGCA
TCAGTTGTTCAAGTTGGTTCCATGTCTGGAAAACAGGATGGGGTGGCAGCATTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT
TCTTAAAACATGTCAACAAGCTGAGTGCCCAGGCGGGTGGCAAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCAGTGCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACGTGACAAAGCAAACGTCAACCACCTGCTTAATGGAGGGACC
TGTTCTACCCCTGGAAAATGTATTGCCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACAACCCCTGTCGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTGCGAGCCTGGCTGGTGCACAT
GGAACCTGCCATGAACCCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGC
ACACGCCTCACTTAAAAGGCCGAGGAGCAGGCCAGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTACAGCTTCAAGTACGTCTGTAG
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATTGTTATTAGCT
TCATTATAAAATCACTGAGCTGATATTACTCTTCTTTAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTCTTCTGTTCAAGTGTAGTTGGCAGATATTTCAAAATTACAATGCATTATGGT
GTCTGGGGCAGGGAACATCAGAAAGTTAAATTGGCAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCAAGATTATTGTCAGATATTAGAT
GTTTGTACATTAAAATTGCTCTTAATTAAACTCTCAATACAATATATTGACC
TTACCATTATTCCAGAGATTCACTTAAATTACACTGTGGTAGTGGCATT
AAACAATATAATATTCTAAACACAATGAAATAGGAAATATAATGTATGAACTTTGCAT
TGGCTGAAGCAATATAATATTGTAACAAAACACAGCTTACCTAATAAACATTAT
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAA
AAAAAAAAAAAAAAAAAGGGCGCCCGACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCAACTGTTATTGCAGCTTATAATG

FIGURE 4

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPOLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKIGSKCKCSKGYQGDLCSKPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW
```

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGCGTCCGGCGTCGAGAGCCAGGAGGCGAGGCCGGCCAGCCTGGG
CCCCAGCCCACACCTCACCAAGGGCCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGCGCCGG
GAGCTAGCACCGGGCTGCACCTGCAGGGCATCCGGACGCCGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGTGCCAGCAGACTGTGCCCTGCCACTGGCGCCATCT
GTTACTGTGACCTCTTGCAACCGCACGGTCTCGACTGCTGCCCTGACTTCTGGACTTC
TGCCTCGGCGTGCCACCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTGCTATCTA
TCCAGTCTGGGAACGTACTGGGACAACGTAAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTCTGGGCATGACCCTGAGGGCATTGCTACCGCCTGGCACCA
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATACTAGTGCTGAACCCAGGGAG
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAAGTGGCCAACCTGATTGAGCCTCTTGA
CCAAGGCAACTGTGAGGCTCCTGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGACACATGACCCCTGTCCTGTCGCCCCAGAACCTGCTGTCTGTGAC
ACCCACCAGCAGCAGGGCTGCCGCGTGGCGTCTCGATGGTGCCTGGTGGTCTGCGTCTG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTCGGCCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCAGGCCATGGTCGGGCAAGCGCCAGGCCACTGCC
CACTGCCCAACAGCTATGTTAAATAACAATGACATCTACCAGGTCACTCCTGCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAAATGGCCCTGCTCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTCCTATAACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACGCCGGCATGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCCAACACTCTGGGGCC
CAGCCTGGGGCGAGAGGGCCACTTCCGCATCGCGCGCGTCAATGAGTGCACATCGAG
AGCTTCTGCTGGCGTCTGGGCGCGTGGCATGGAGGACATGGTCATCACTGAGGCTG
CGGGCACACGCCGGTCCGGCTGGATCCAGGCTAAGGGCCGGCGAACAGGCCAACATG
GGCGGTGACCCAGCCTGCCGACAGAGGCCGGCGCAGGCCGGCGCAGGGCGCTAAT
CCCGCGCGGGTCTCGCTGACGCAGGCCCGCTGGAGGCCGGCAGGCCGAGACTGGCG
GAGCCCCAGACCTCCAGTGGGACGGGCAGGGCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCTCTGGGCCCTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCAACTCCGTATTCTTTTTTTTTAGACAGGGCTTGCTCC
TTGCCAGGTTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACCTCCGACTCCTGGTTCA
AGTACCCCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCAACACCTGGC
TAATTTGTATTTGTAAAGAGGGGGCTCACTGTGTTGCCAGGCTGGTTGAACT
CCTGGCTCAAGCGGTCCACCTGCCTCCGCCTCCAAAGTGCAGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCAAGATATTATTTCTTCACTGTTTTAAAAA
TAAAACCAAAGTATTGATAAAAAAAA

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYEQDLCCRGRAADD
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWILAGWEHQQLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTNTGCNATCCCGATTGTTGTCTCAAATCCA
ATTCTCTGGGACACATNACGCCTGTCCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCTCGTGCCTGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGGGGCAAGGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCTCG
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTCTTCCATACAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACC CGCGCATCCCGCGAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAAC TGC GTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCA GTGGGAGCCTGTCCTGGTTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCTGACCCCTCCATGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCTCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTTAACCCTGTGCTCAGGCACCTCTCCCCCAGGAAGCCTT
CCCTGCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGCCAGGCCTCACATTGTTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCCFHGPAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCACCGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCGCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAAACCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGTGGAGAACAACTATACGGCCTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCGCAGGGCGGCCAGGCTCCGCAGCCGCCAGAAC
CAGCGCGAGGCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAACGAGAACAGCTGAGTTGTGGCTCCGCCACCCGCCAGCAAGCGCACAC
GGCGGCCAGCCCTCACGTAGTCTGGGAGGCAGGGGCAGCAGCCCTGGGCCCTCCC
CACCCCTTCCCTTCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGAGCCAGATCCCC
GAGGGAGGACCTGAGGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCTTCCGGACGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCTCCAGCCGGCTCTGAAGCC
CGCTGAAAGGTCAAGCACTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCACCCAGCCCCAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTCAAGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCCCACCCCAACTCCCAGCCC
CGGAATAAAACCATTTCTGC

FIGURE 11

MGAARLLPNLTLCQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRR
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKD
VFEIVLENNYTAFQNARHEGWFMAFTRQGRPROASRSRQNQREAHFIKRLYQGQLP
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCATCACCTGTCAGTGGAAAAATTCTCCCTGTTGAATTTGCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCATCCAGT
CATTTGATTTGCTGTTATTTTTCTTTCTTTCCCACACATTGTATTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTCT
GAAGTCTTGGCTTATCATTCCCTGGGGCTACTCACAGGTGTCAAACCTCTGGCCTGCC
CTAGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCCAGGGCGTAACCGTACTCTACCTCCACAACAAACAAATTAAATGC
TGGATTCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTCCAAGAACATGTCAGAGTTCTCCATTGCAGGAAAAC
AATATTCAAGACCATTTCACGGGCTGCTCTGCCAGCTCTGAAGAGCTGACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCCTCCGGGAGGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAACATCACCTGAGCAGTGTGCCTGTTGGCTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAATCGAATTGCTGTCAATCCGACATGGCCTCCAGAA
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGAACCTCCTGACCAACAAGGGTATCGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTACGTAATTGCTGTCC
CACCCCTCCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAGGACAACCAGAT
AAACCACATTCTTGACAGCCTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGTTTGATAATCTCTCCAACCTGAAGCAGCTC
ACTGCTCGGAATAACCCTGGTTTGACTGCAGTATTAAATGGTCACAGAACATGGCTCAA
ATATATCCCTTCATCTCAACGTGCGGGTTTCATGTGCCAAGGTCTGAACAAAGTCCGGG
GGATGGCCGTCAAGGAATTAAATATGAATCTTGTCCCTGACCAACTCAGCCTCCCACCCTCTAT
CCTCTCTCACCCAGCCCCAAGTACAGCTCTCCGACCACTCAGCCTCCACCACATCGAAACTCCACGATT
CTGACTGGGATGGCAGAGAACAGTGAACCCACCTATTCTGAACGGATCCAGCTCTCTATC
CATTGTTGAATGATACTTCATTCAAGTCAGCTGGCTCTCTTCACCGTGTGGCATA
CAAACACATGGGTAAAATGGGCCACAGTTAGTAGGGGGCATCGTTCAGGAGCGCATA
TCAGCGGTGAGAACACCTGAGCCTGGTTAACCTAGAGCCCCGATCCACCTATCGGATT
TGTTAGTGCCTGGATGCTTTAACTACCGCGCGGTAGAACAGACACCATTGTTCAGAGGC
CACCAACCATGCCTCTATCTGAACAAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATT
GTGCTGGTGGTCTGCTCAGCGTCTTGCTGGCATATGCACAAAAAGGGCGCTACACCTC
CCAGAAGTGGAAAATACAACCGGGCCGGCGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTCAGATCGTCTCTAAATAACGAT
CAAACCTTAAAGGAGATTTCAGACTGCAGCCCATTACACCCAAATGGGGCATTAATT
CACAGACTGCCATATCCCCAACAACATGCGATACTGCAACAGCAGCGTGCAGACCTGGAGC
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCAGAACATTAGACTCTTGAGAA
CACACTCGTGTGCACATAAGAACACGCAGATTACATTGATAAAATGTTACACAGATGCAT
TTGTGCATTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAAAGTG
CTATCTTTCTATTCAAGTTAACAGTTGTAACCTTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGAFFLKSLLIISLGLYSQVSLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLDNSISTVGVEDGAFREAIISLKLFLSKNHLSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELMNLLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTSKLPTIPDWDGRERVTPPISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGCGGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCCGCTCCACGAGCG
ATCCCCGAGGAGAGCCGCGGCCCTCGCGAGGCAGAGGCGACGAGGAAGACCCGGGTGGCTGCGCCCTGCC
TCGCTTCCCAGGCAGGCCCTCGGACAGATCGTCCTCCTCCCTGCCAGGGCAGGGAGCGGTACGTGGAGGTCCATCT
CTAGGGCAGACACGCTCGGACCCACCCGAGACGGCCCTCTGGAGAGTCCTGTGAGAACAAAGCAGGGCAGACC
TGGTTTCATCATTGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA
TCTTGCAATTCTGGACATTGGCCTGATGTCACCCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAATG
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGTGCTCAAGAGGATGCGGCATCTGTCCACGG
GCACCATGACTGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAACAGCAGAGGGGGCCGGCCCTGA
GGGAGAATGTGCCACGGTCATAATGATCGTACAGATGGAGACCTCAGGACTCCGTGGCCAGGTGGCTGCTA
AGGCACGGGACACGGGCATCTAATCTTGCCATTGGTGTGGCCAGGTAGACTTCAACACCTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCCTCCTGTGGCCAATTCAAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGCACGGCCCACATGTGCAGCACCCCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTG
GCTCATACTGCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAACATCCAGGATCTGT
GTGCCATGGAGGACCACAACGTGAGCAGCTCTGTGAATGTGCCGGCTCCTCGTCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGACTACTGTGCCTCAGAAAACCACGGATGTGAAC
ATGAGTGTGAAATGCTGATGGCCTACCTTGCCAGTGCATGAAGGATTGCTCTTAACCCAGATGAAAAAAA
CGTGCACAAGGATCAAAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCAGTGGACCACTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGAACACACGGAGGATTCCCTCGTCTGCCAGTGCTCAGAACAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGCTCCGGGTGGATTACTGCCTGCTGAGTGAACATGGTTGTGAATACTCCT
GTGTCAACATGGACAGATCCTTGCCTGTCAGTGTCTGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTG
CAAAATTGGACTCTTGTGCTCTGGGGACCACGGTTGTGAACATTGCTGTAAGCAGTGAAGATTGCTTGTGTT
GCCAGTGTGTTGAAGGTTATAACTCCGTGAAGATGGAAAAACCTGCAGAACAGGAGATGTCTGCCAAGCTATAG
ACCATGGCTGTGAACACATTGCTGTAACAGTGCAGACTCATACACGTGCGAGTGCTTGGAGGGATTCCGGCTCG
CTGAGGATGGAAACGCTGCCAGGAAGGAAGGATGTCTGCAAATCAACCCACCATGGCTGCGAACACATTTGTGTTA
ATAATGGGAATTCTACATCTGCAAATGCTCAGAGGGATTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAAAT
GCACTGAAGGCCAATTGACCTGGTCTTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTGAGGTGCG
TGAAGCAGTTGTCACTGGAATTATAGATTCCCTGACAATTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTCAACTCAGCCAAAGACATGAAAAAAAGCCGTGGCCC
ACATGAAATACTGGAAAGGGCTCTATGACTGGCTGGCCCTGAAACACATGTTGAGAGAAGTGTACCCAAAG
GAGAAGGGCCAGGCCCTTCCACAAGGGTCCCAGAGCAGCCATTGTTCTAGCGACGGACGGCTCAGGATG
ACGTCTCCGAGTGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG
AGGAGGAACATACAAGAGATTGCCTCTGAGCCCACAAACAAGCATCTCTTCTATGCCAGAACAGACTCAGCACAATGG
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAACAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAACGCCAAAAACGGTCCAACAGCCAACAGAACATGAGCCAGTCACCATAAATATCCAAGACCTACTTT
CCTGTTCTAATTGCACTGCAACACAGATCTGTTGAAGAACAGAACATCTTACGGTCTACACAAAAGCTTT
CCCATTCAACAAAACCTTCAGGAAGCCCTTGGAAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCAACAGAACAGTAAGAAAATTAAACACAGCGCTTAGAACAGAACAGAGAACGGGCT
TGGAAAATCGCCTGAGATAACAGATGAAAGATTAGAAATCGCGACACATTGTTAGTCATTGTATCACGGATTACAAT
GAACGCAGTGCAGAGCCCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGAAGTAAAACAATCAGTACTGA
GAAACCTGGTTGCCACAGAACAAAGACAAGAACAGTATAACTAACACTTGTATAAATTCTAGGAAAAAAATCCT
TCAGAATTCTAAGATGAATTACCGAGGTGAGAACAGAACAGAACAGAACAGAACAGAACAGAACAGAAC
AACTTGCTTCTGCCTCATCCTGCCTTAGTGTGCAATCTCATTGACTATACGATAAGTTGCACAGTCTTACTT
CTGTAGAACACTGCCATAGGAAATGCTGTTTTGTACTGGACTTACCTTGATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTATAACAATATTAAAATTCACCACTTCAG

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRHARTHPTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAEGRPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIQVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLSVFQKKLCTAHMCSTLEHN
CAHFCINI PGSYVCRCQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNPGC
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTCAKLDSCALGDHGCE
HSCVSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIHGCEHICVNSDDSYTCECLEGFR
LAEDGKRCRCKDVCKSTHGCEHICVNNNGNSYICKCSEGFLAEDGRRCKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKA
GITMYAVGVGKAIEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGGGCTGGCGCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTCCCTCCGGGCCCCCTGGTACCAACTTGCTGCGGTTTGTCTGGGCTGA
GTGCCCTCGGCCCTCGCGGGCCCAGCTGCAACTGCACCTGCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTGCTCCAGCGTGGTACACCTGCACGGGAGGTGTCTC
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGTACAAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCCTGGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTCAAGACAAACAAGGCAAATCTAGGGCACAGCATAAAACCT
TAGAACTCAATGTAAGTGGTCCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCCAATACCA
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCCAGCATTAGATGTCATCCGTG
GGTCTTAAGCCTCACCAACCTTCTGCTTCCATGGCTGGAGTCTATGTCATGCAAGGCCAC
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTTGGTACCCCTGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCACCGCCGGCAAGGCCCTGGAGGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAACGGACCCT
TTCCTCTGTCACCTCCGCACGAGCCCTCCGCCACCCATGCCCTCCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCCTGCCAGAGTCAAGCTGGCTCTGGTAT**GATGAC**
CCCACCACTCATTGGCTAAAGGATTGGGCTCTCCTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTCCAGTCAGTCTCCAGGC
CCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGCAGAGGATAGGAAATCTC
TTATTAACATGAAATATGTGTTTTCAATTGCAAATTAAATAAGATAACATAA
TGTTGTATGAAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLP AWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEG LQEKDGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTACQCNVTLEVSTGPGAA
VVAGAVVGTTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTL PWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPS PRLPTTDGAHPQPISPIPGVSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCGCTCCTAGTGGTTTTCCACTTTG
TTGAATTGTTCTATACTCAAAATTGCACCAAGACACCTGCTCCCAAATGCAAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACCAA
TTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGTCCTGTGGCGAAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGCCATT
TAGATAATGTCTGTATAGCTGCAAATATTAAATAAAACTTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAAACA
CTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTTACTGAATTGTAAGGACCGTGAAT
AATTTGTTCAAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTCTTTGAT
TCATATAACATGAAACATATTCATCCTCATATGAATATGGATGGAGACTACATAAATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATA
AGAGTATTGGCCTTGCTTCATCATCTGACAACCTTCTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATGAACCTGAAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCATTGGATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATT
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGTCTTGCATATGCATT
ACCTTCTGGTTCTTCAGTCAAAGCACCAGGACAACAATTCAAACAAATTCTTGTGCTG
TAGCCTATTCTTGTGAACTTGTGTTGGATCAATACAAACTAATAAGCTCT
TCTGTTCAATCATTGCCGACTGCTACACTACTTCTTTAGCTGCTTGCATGGATGTGC
ATTGAAGGCATACATCTATCTCATTGTTGGTGTCACTACAACAAGGGATTGGCA
CAAGAATTTTATATCTTGGCTATCTAACGCCAGCCGGTAGTGGATTTCGGCAGCAC
TAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCGAAAACAACCTTATT
TGGAGTTTATAGGACCAGCATGCCATTCAACTCATTGTTAATCTCTGGCTTGGAGTCAT
CATATACAAAGTTTGTACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTGAGAAC
TAAGGTCTTGTGCAAGAGGAGGCCCTCGCTCTGTTCTCGGACCAACTGGATCTT
GGGTTCTCCATGTTGTGCACGCATCAGTGGTTACAGCTTACCTCTCACAGTCAGCAATGC
TTTCCAGGGGATGTTCAATTCTTGTGTTGTTATCTAGAAAGATTCAAGAAC
ATTACAGATTGTTCAAAAATGTCCCCTGTTGGATGTTAAGGTAAACATAGAGAAC
GTGGATAATTACAACACTGCACAAAATAAAATTCCAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCCAATTATTAACACTAGACAAAAGTATTAAATCAGTT
GTTTATGCTATAGGAACGTAGATAATAAGGTAAATTATGTATCATATAGATATACTATGT
TTTCTATGTGAAATAGTTCTGTCAAAATAGTATTGCAGATATTGGAAAGTAATTGGTT
CTCAGGAGTGTATCATGCACCCAAAGGAAAGATTCTTCTAACACAGAGAAGTATATGAA
TGTCTGAAGGAAACCACTGGCTTGATATTCTGTGACTCGTGTGCTTCAAAC
CCTACCACCTCGGTAAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAAC
ATATCAAACAGTGAAAAGGAATGATAAGATGTATTGAAATGAACTGTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAACACATTACCA
TTGTTCTGAACCTAAATGTCCACTAAAACAACCTAGACTCTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEYRNSVTDLSPTDIITYIEILAESSSLGYKNNTISAKDTL
SNSTLTEFVKTVNPFVQRDTFVWDKLSVNHRRTHLTKLMHTVEQATLRIQSFKTTEFDT
NSTDIALKVFFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSNGNVAVALYYKSIGPLLS
SSDNFLLPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITYFTLSHRKVTDRYRSLCAF
WNYSPDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIAGL
LHYFFLAAFAWMCIEGIHLYLIVVVIYNKGFLHKNFYIFGYLSPA VVGFSAALGYRYYGT
TKVCWLSTENNFIFSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTTGATGTCCTCTGGTCCTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCTCCGCAGATCCGAACGGCCTGGCGGGGTACCCCGCTGGGA
CAAGAACGCCGCCTGCCTGCCCGGGCCGGAGGGGGCTGGGGCTGGGGCCGGAGGGGG
GGTGTGAGTGGGTGTGCGGGGGCGGAGGCTGATGCAATCCGATAAGAAATGCTCGGG
TGTCTGGGCACCTACCGTGGGGCCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCCTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGCCACGACCATCCAACCC
GGCACTCACAGCCCCCAGCGCATCCGGTCGCCGCCAGCCTCCGCACCCCCATGCCGG
AGCTGCCGAGAGCCCCAGGGAGGTGCCATGCCGGAGCGGGTGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCGGGCGCCCGCTGCCCTCTCGGACGCCGGGCC
CCACGTGCACTACGGCTGGGGCAGCCCATCCGCCTGCCACCTGTACACCTCCGGCC
ACGGGCTCTCCAGCTGCTCCTGCATCCGTGCCACGGCGTCGTGGACTGCCGGCGGG
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCCAGCGTGGCCATCAAGGG
CGTGCACAGCGTGCCTGACCTCTGCATGGCGCCACGGCAAGATGCCAGGGCTGCTCAGT
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAACGCCCTCCGGCTCCCTGAGCAGTCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTCTCCACTCTCTCATTCCTGCCATGCTGCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCCAGCTTGAGAAGTAA
GAGACCATGCCGGGCCTCTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG
TGCTTCTACAAGAACAGTCCCTGAGTCCACGTTCTGTTAGCTTAGGAAAGAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTCCAGTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTGCCAGCTGCTGGCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTGAATACCTCCATCGATGGGAAC
TCACCTCCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTCATCACTTC
CCCAGGAGCAGCCAGAACAGACAGGAGTAGTTAATTCAAGGAAACAGGTGATCCACTCTGTA
AACAGCAGGTAAATTCACTCAACCCATGTGGAAATTGATCTATCTACTTCCAGGG
ACCATTGCCCTCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGCCACCAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTGAGAATTCCCC
CTGAGGCCAGTTCTGTCACTGGATGCTGCTGAGAATAACTGCTGTCCCAGGTGACCTGC
TTCCATCTCCAGCCCACCAGCCCTCTGCCACCTCACATGCCCTCCCATGGATTGGGGCCT
CCCAGGCCCCCACCTTATGTCAACCTGCACCTTCTGTTAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTGTCAATAACTGCTGTGGAAAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCAGCACTGGTTCCAACATGATATTATGAGTAATTATTGATATGTACA
TCTCTTATTCTTACATTATTATGCCCAAAATTATATTATGTATGTAAGTGGAGTTG
TTTGTATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHLRPLVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCCGGGAAAGATGGCGAGGAGGAGCCACCGCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTCTGCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCCAA
AGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACTGACTCTGGAAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA
ATCCCAGACTTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAAACTGGAACT
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCGCAATT
TGTGGATATCGCAGGTGCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTCCGTTGTGGCCTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTGGAAATGTGCAGTGGCTACGCCTGTAATCCCAGCACTTGGAAAGG
CCGGCGGGCGGATCACGAGGTCAAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGCGCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAACCCGGGAGGCAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAAATAAAATAATA
AATAAAATCTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLRLYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAI LACKTPKKT
VSSRLE WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD
GIRLLENPRLGSQST NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN
SVGYRRCPGKRMQVDDLNI
SGIIIAVVVVA LVISVCGLGV
CYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPV
IPALWKA
AAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTTATTAACATGCTCCACAGCCGGACCCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGATTAAATATTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCACATCTACATACTCCACCTCAAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTCTCTCTCCAAATATGCATGACATTGGACAAATG
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGGTTCTATGGCATTCA
TTGACAAATGCAAGCATCTCCTTATCAATCAGCTCCTATTGAACCTACTAGCACTGACTG
TGGAAATCCTTAAGGGCCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCAATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTAACTTTCCAGCCAGATTGCC
AGCTAACACACAGATTCTCTCCTACAGACTAACAAATATTGAAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTATCTCAGTCACCAAT
ATTAATGTAAAAAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTTACTGA
ACTGCCTGAAAAATGTCTGTCCGAACGTGAGCAACTTACAAGAACTCTATATTAATCACA
TGCTTCTACAATTCACCTGGAGCCTTATTGGCTACATAATCTTCTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTATCAGAATCAAAGACATGAACTTAAAGCCTCTTATCA
ATCTCGCAGCCTGGTATAGCTGGTATAAACCTCACAGAAATACAGATAACGCCCTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCATGT
TGCTCTTCAAAAAGTTGTAATCTCAAATTGGATCTAAATAAAATCCTATTAATAGAA
TACGAAGGGGTGATTTAGCAATATGCTACACTAAAAGAGTTGGGATAAAATAATATGCC
GAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTAAAGAAAAATAGAAGC
TACTAACAAACCTAGATTGTCTTACATTCAACCCAAATGCATTTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCATCAGGTGTACTGTGATCCGTTG
GATGAACATGAACAAACCAACATTGATTCAATGGCCAGATTCACTGTTTGCCTGGACC
CACCTGAATTCCAAGGTAGAATGTTGGCAAGTGCATTTCAGGGACATGATGGAAATTG
CTCCCTCTTATAGCTCCTGAGAGCTTCCTCTAAATCTAAATGTAGAAGCTGGAGCTATGT
TTCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTG
GTCAAAAACCTTGCCTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA
GATATAATGGCGTAACCTCCAAAGAAGGGTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG
GCTCTTGAATATTAAGAGATATTCAAGGCCATTCAAGTTGGTGTCTGGAAAGCA
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTCGCAAAGTGCCTGAATACCACATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCCACCATCTACAGAAAAACAGAAAAAAA
TGTGTAAATGTCAACCACCAAGGTTGCACCCCTGATCAAAAAGAGTATGAAAAGAATAATAC
CACAAACACTTATGGCCTGTCTGGAGGCCTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCCTGTATAAATCTCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTACCAACAAATATGTCC
AAAAACCAAGGAAACCTACTCCAAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRLSIVAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVNLKFQFLDNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESIMLNSNALSALYHGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNI RFMEPDSLFCVDPPEFQGQNVQHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHC RATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC
IATNLVGADLKSVMIKV DGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTLMACLGGLGIIGVICLISCLSPEMNCDGGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCGGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTGTTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCTCCAAGGGCTGTCTTGTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGGCAGAATTGCCAACAAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTGGCTGGTTCACTATGGTATCTCATATGTGGTATATTATGTGAGGAAAATCAGGAG
GATGCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTGCGATTGCAGTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACATTGAA
ACTTTGTATTCAGTTTTGAATTATGCCACTGCTGAACCTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAATAATGAAATTATTTTTT
AATTAAAAGCAAATAAGCTTAACTTGAACCAGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMC PKGCLSSGGLNVTC SANLKEIPRDL
PPETVLLYLDNSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGGCATGCCAGCCCCCTGGCCTGCTGGCAGCCCATTCTCCTGCTGGTGCT
GGGCTCAGTGCTGTCAGGCTCGGCCACGGCTGCCGCCGCTGCGAGTGCTCCGCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTCGCCAG
CTTCCCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGGCCGTGGAGGCCGGCG
CCTTCAACAACCTCTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC
CCGCTAGGCGTCTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCGCGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCTGTCCCACCTGCACGGCCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTCAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCCTACTGGACACCATGACACCCAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCACCTCTCCTACAAACCCATCA
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGC
GGCAGCTGGCGTGGAGCCCTATGCCCTCCGCCCTCAACTACCTGCGCTGTCAA
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCCTGTGGGTGTTCCGG
CGCCGCTGGCGGCTCAACTCAACCGGCAGCAGCCCACGTGCGCCACGCCAGTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCAACTACTTCACCTGCCCGCG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGGCACACGGTGCAGTT
GTGTGCCGGGCCATGGCGACCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGGCGGCAACGAC
TCCATGCCGCCACCTGCATGTGCGCAGCTACTGCCGACTGGCCCCATAGCCAACAA
GACCTTCGCTTCATCTCCAACCAGCCGGCGAGGGAGAGGCCAACAGCACCGGCCACTG
TGCCTTCCCCTCGACATCAAGACCTCATCATGCCACCAACATGGCTTCATCTCTTC
CTGGCGTCGTCCTCTGCCTGGTGCTGCTGTTCTGGAGGCCGGCAAGGGCAACAC
AAAGCACAACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCG
ACGCGCCCCGCAAGTTAACATGAAGATGATATGAGGCCGGGGCAGGGACCCCG
GGCGGCCGGCAGGGGAAGGGCCTGGCGCCACCTGCTCACTCTCAGTCCTTCCACCTC
CTCCCTACCTCTACACACGTTCTTTCTCCCTCCGCCCTCCGCTCCCTGCTGCCCG
CCAGCCCTCACCAACCTGCCCTCTTCTACCAAGGACCTCAGAACGCCAGACCTGGGGACCCCA
CCTACACAGGGGATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTCA
ATAATTCAATAAAAAGTTACGAACCTTCTGTAACCTGGTTCAATAATTATGGATTT
TATGAAAATTGAAATAATAAAAAGAGAAAAAAACTAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYRLFLNLSYNPISTIEGSMLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVNVSGNQLTTLEESVFHSVGNLETLILDSNPLA
CDCRLLWVFRWRRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCACCGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGGATTCAAGGCTGCCAGCGCCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGC
TGTCGCCTGCTGCTGGCGCCGGCGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGCACCCTGGTCAAGTCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTACTTTGGGAGAAGA
GAGCCCTCGAGATAATCGAATTCAAGCTGGTACCTCTACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT
ATAAAATCTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTTCTGGGAGCAAG
CCTGCAGCCGGCTCACCTGGAGAAAGGGTACCAAGAACCTCACGGAGAACCAACCGCAT
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCCTGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAACGCTGTGCTACACTGTGAGGGTCGCCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAACGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
AACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT
CCTCCTCCAGCACCTACCACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTCCTGGCCACTACTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTCATAGAGGCGCTGCCACTCCTGC
GCCCCCCAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC
TTGGGTGCGGTTTGACTCGGTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGGCCCTGGGTGAGAAAAGCAAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLFAACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTCTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAAATGCTGCTTGGATTCTGTT
GCTGGAGACGTCTTTGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGT^{TT}ACCA^{TT}CTGCATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTTGCTAACCTTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTCTGGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAACAACAAGATCAAGTCTTCGAAAGCAGACTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTACGAGATATAGACCCGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTAAATGACAATCTCATCAGCACCC^{TT}ACCTGCCAAC
GTGTTCCAGTATGTGCCATCACCCACCTCGACCTCCGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCACAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCCTTGAAAAACCGAGTGGATTCTAGTCTCCGGGCCCTG
CCCAAGAACAGAGACCTTGCTCCTGGACCCCTGCCA^{CT}CC^{TT}CAAGACAAATGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
AAAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCCTAGCTAAC
GTTTACCC^{CT}GCC^{CT}GGGGCTGCAGCTGCGACCACATCCCAGGGTGGTTAAAGATGAAC
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAGGA
GCTTTCC^{CT}ACGAGATAACAAGATCCACAGCATCCGAAAATCGCA^{CT}TTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTTCAAG
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCC^{GG}GA
GAAATT^{CG}GGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCC^{GG}GCAC^{TT}CAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAAACACTG
CTGAGGTCCCTGCC^{CT}GGACGTGTCGCTGGGTCTCGCTCTAAACTCAGC^{CT}GCACAA
CAATTACTTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCC^{CT}GGGAGTGCTCCTGCACAATTGTGCCTTCAAGCAGTGGCA
GAACGCTTGGGTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAAC^{TT}CTT
TAGAAAGGATTTCATGCTCCTCCAATGACGAGATCTGCC^{CT}CAGCTGTACGCTAGGATCT
GCC^{CC}ACGTTAAC^{TC}CGCACAGTAAAAACAGCACTGGGTGGCGAGACCGGACGCAC^{TC}
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCC^{GG}ACTGCTGTT
GTTGTCACCTCCGC^{CT}TCACCGTGGTGGC^{AT}GCTCGT^{TT}TATCCTGAGGAACCGAAAGC
GGTCCAAGAGAGCAGGAGATGCCAACTCCTCCGGTCCGAGATTAAATTCC^{CT}ACAGACAGTCTGT
GA^{CT}CTTCC^{CT}ACTGGCACAATGGGC^{CT}TACAACGCA^{GT}GGAGACGGCCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACT^{AA}GGACCC^{CA}ACCC^{CA}ATAGGGAGGGCAGAGGGAAAGGCG
ATACATCCTTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCC^{AA}ATCCCCGCG
CCATCAGCCTGGATGGCATAAGTAGATAAAATAACTGTGAGCTCGCACAACGGAAAGGGCCT
GACCC^{CT}TACTTAGCTCC^{CT}CTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCT^{TT}GCTGAGAGCC^{CT}TTGACAGAAAGCCCAGCAGCAC^{CC}CTGCTGGAAAG
AACTGACAGTGC^{CC}CTGCC^{CT}CGGCCCCGGGC^{CT}GTGGGGTTGGATGCC^{CG}GGTTCTATAAC
ATATATA^{AC}ATATCCACATCTATATAGAGAGATAGATCTATT^{TT}CC^{CT}GTGGATTAG
CCCCGTGATGGCTCC^{CT}GTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAAC^{TT}GACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPG AFLGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRIDPGAFQDLNKLLEVILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPLYEEVLEQIIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTFKTNGQEDHATPGSAPNGGT
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGCSDHI PGSGLKMCNNRNVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLLDGNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNALIQLILPGTFNAMPKLRILILNNNLLRSLPVDFAGVSL
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHNSYLDTSRVSISVL
VPGLLLVFVTSAAFTVVGMLVFILRNRKRSKRRDANSSASEINSLQTVCDSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCTGTACCCGGGCCAGCTGTCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCTCTGCGCCCTAAGGGAAACTGTTGGC
CGCTGGGCCCGCGGGGGATTCTTGGCAGTTGGGGGTCCGTCGGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCAGGGCCTCAG
AGAATGAGGCCGGCGTCGCCCTGTGCCTCTGGCAGGCCTCTGGCCGGGGCCGGCG
CGCGAACACCCCACGTGCCGACCGTGCTGGCTGCTCGGCCTCGGGGCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGGCGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC
AGCACC GTGCGTGCAGCGCCGAGCTGCGCCTGTGCTCGCCTCTGCGGGCAGGCCAGG
GCCCGGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTCGCACTGGAGCGCAGGCCTCCACT
GCACCCCTGGAGAACGAGCCTTGCGGGGTTCTCCTGGCTGTCCCTCCGACCCCGGGGTCTC
GAAAGCGACACGCTGCACTGGGTGGAGGAGGCCAACGCTCCTGCACCGCGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAAGCTTGAGGTCTTGTGTCCTGCGCCGCCGG
GCCGCCTCTAACTTGAGCTATCGCGCCCTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTCCCTGCC
GGGAGGTACCTCCGTGGCAAATGCGCAGAGCTCCACTGCCTAGACGACTTGGGAGG
CTTGCGCTGCGAATGTGCTACGGGCTTCGAGCTGGGAAGGACGGCCGCTTTGTGACCA
GTGGGGAGGACAGCCGACCCCTGGGGGACCGGGGTGCCACCAGGCGCCGGCCACT
GCAACCAGCCCCGTGCCGAGAACATGGCAATCAGGGTCGACGAGAACAGCTGGGAGAGAC
ACCACTGTCCCTGAACAAGACAATTCACTAACATCTATTCTGAGATTCTCGATGGGAT
CACAGAGCACGATGTCTACCCCTCAAATGTCCCTCAAGCCGAGTCAGGCCACTATCACC
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTT
CGACTCCTCTGCCGTGGTCTTCATATTGTGAGCACAGCAGTAGTAGTGTGTTGGTATCT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCACGAAAGCCCTCTCCAGCCA
AGGAAGGAGTCTATGGCCCGCCGGCCTGGAGAGTGATCCTGAGCCGCTGTTGGCTC
CAGTTCTGCACATTGCACAAACAATGGGTGAAAGTCGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCTGCTGGCGAGTCCCCTCTGGCTCTAGTGATGCATAGGGAAACAGGGAA
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACAGGGAAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAGTGCCTTAGGA
TGGTGATACTGGGGGACCGGGTAGTGCTGGGAGAGATATTCTTATGTTATTGGAGAA
TTTGGAGAAGTGAATTGAACTTTCAAGACATTGAAACAAATAGAACACAATATAATTACA
TTAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTGAAATCCCAGGGAAAAAATAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGL
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPG
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILTMVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTCAAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGAAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCCTTAAAAGTGCCTCCGCCCTGCCGGCGTATC
CCCCGGCTACCTGGGCCCGCCGGCGGTGCGCGCGTGGAGAGGGAGCGCGCGGAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGTGTGAGCGCGGTGGGTGCAGGA
GGGGCGTGTGTGCCGGCGCGCGCCGTGGGTGCAAACCCGAGCGTCTACGCTGCCATGA
GGGGCGCGAACGCCTGGCGCCACTCTGCCTGCTGCTGGCTGCCACCCAGCTCTCGCG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGGAAAATCA
CAGTCCCCGAAGGAAAAGTAGCGTCTCAATTCCGATTCAAGACCTCGAGAGTACAAC
CTGTGCCGCTATGACTTGTGGATGTGTACAATGGCCATGCCAATGCCAGCGCATTGGCG
CTTCTGTGGCACTTCCGGCCTGGAGCCCTGTGTCCAGTGGCAACAAAGATGATGGTGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTTCATGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTCTTTAAAAC
CCCCAACTGGCCAGACCGGGATTACCCCTGCAGGAGTCATTGTGTGGCACATTGTAGCCC
CAAAGAACATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTTTAATGGGGGGAAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGTAGTCCACCTGCCATTGTGTCTGAGAGAAATGAACCTCTTATTCACT
TTTATCAGACTTAAGTTAACTGCAGATGGTTATTGGTCACTACATATTCAAGGCCAAA
AAACTGCCTACAACACTACAGAACAGCCTGTCACCACATTCCCTGTAACCACGGTTAAA
ACCCACCGTGGCCTGTCAACAAAAGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAACCACACTCGCGATGGAGTTG
CACGCCACAGTCTCGATCATCACATCTACAAAGAGGGAAATTGGCGATTAGCAGGCCGG
CAAGAACATGAGTGCAGGCTGACTGTCGTCTGCAAGCAGTGCCTCTCCTCAGAACAGGTC
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGCAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAACATCAGAACAGCTCCTGGATGCCATTGAAAGATCTATGTT
TTAACAGTGAACGTGTCCATTAAAGCTGTATTCTGCCATTGCCATTGAAAGATCTATGTT
TCTCAGTAGAAAAAAATACCTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAAGTTCT
TGCCTGCTGTCAGAGGAGCAGCTATGATTGGAAACCTGCCACTTAGTGCAGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAAGCGTTATTATACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTTAGAAGTGCAATATTATAGT
GTTATTGTTCACCTCAAGCCTTGAGGTGTTACAATCTGTCTTGCCTTCTA
AATCAATGCTTAATAAAATATTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTRDGSLHATVIINIVKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMQVGVEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCCGGGCTGGGCGGTGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGACAACACTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAACATTGTCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGAACAGAGAGGCCCTGCGGTGGTACGGGCAGTGTGAAGGAGAACCG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGTACGGGGTGAGGCCTGTTGCC
AGTGTGGCCTTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAACGG
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAAC
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGGCCAGGTGCGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA
ACAAGCAGTGTAAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCAGCAGATGTTCTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTCAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGA
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCGAGAGCTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTGGTTATTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTCACCTGGCGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTCCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCTGCCAGTTCTGT
TCTGTGTTACACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLESELVESWWFHKQ
QEAPDLFQWLCSDSLKLCGPAGTFGPSCLPAGGTERPCGGYQCEGEGTRGGSGHCDQAG
YGEACGQCGLGYFEAERNASHLVC SACFGPCARCSGPEESNCLQCKKGWALHHLKVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKCSPGYQQVGSKCLDVDECE
TEVCPGENKCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWL SERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTGCTCCTCCAGGGCA
GCACCATGCAGCCCCTGTGGCTCTGCTGGGCACCTCTGGGTGTTGCCCTGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTCAGCTCAAAGAGGT
GCCAACCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACACTGCTGGTGTTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCAGCTTCCAGG
AGCCGGTCCCCAAGGCCCGCTGCACAGGCACGGCGGCTGTCCCCCGCGAGCGCCCGGGCC
CGGGTGACCGTCGAGTGGCTCGCGTCCCGACGACGGCTCCAACCGCACCTCCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCTCGCAGGGGGC
GCCAGCCGGCTTGGGAGGCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCCGGGCTT
CCTGGCTTATGAGTGTGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTCAAGTGGC
CGTTCTGGGCCTCGACAGTCATGCCCTCGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCCTCGGATGGTGCCTCGTGCCTGCCAAGGAGGCTCCAGCCATAGGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTGCAGGGTACCAAGGAGAGCTG
GCGATGACTGAAGTGCCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTGGCTCTCAGGAATGAGAATCTTGGCCACTGGA
GAGCCCTGCTCAGTTCTATTCTTATTACTGCACTATATTCTAACACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTACTTGTCCGTAC
TGGATCTGGCTAAAGTCCTCCACCACCTCTGGACCTAACGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTGTAAAACATGAATAAACACATTTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFSREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQVSQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAAAGTTGACCA
AGGAGACACCACCACTCGTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTGCCAACCTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATAACACCTGGTTCAAAGAT
GGGATAGTGTGCCTACGAATCCAAAAGCACCCGTGCCTCAGCAACTCTCCTATGTCCT
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCCTGTCACTGATACTGGAGAATACA
GCTGTGAGGCACCGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCCCTGGTGTGAGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCTTATTGTCTTC
TACACCCCACAGGGCCCCCTACTTCTCGGATGTGTTTAATAATGTCACTGCTATGTCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACTGTTAAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGAAAAATGGCGGGGTGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTTCTGGCTCTTCTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGAAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG
TGATGACACTGGGGCCTTCATCTCTGGGGCCCCTCTCTGTCTTCCCCTGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCCCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTTGTGGAGAGCAGTAGTAAATTTCAGAGAACTGAAAGCCAAAAG
GATTAAAACCGCTGCTCTAAAGAAAAGAAAAGCTGGAGGCTGGCGCAGTGGCTCACGCCTG
TAATCCCAGAGGCTGAGGCAGGCAGGATCACCTGAGGTGGAGTCAGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILA ILLCSLALGSVTVHSSEPEVRI PENNPKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLT CSEQDGSPPSEYTWFKDGI VMPTNPKSTRAFSNS
SYVLNPTTGE LVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTCCCCACCCACCAAGTTCCAGTGCAGCACCAGTGGCTATGCGTGCCCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCAACGCCCTGGCCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCAGCTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCACCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCCTCTGCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACGCCACCCCTCCTCCTTGTCCCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC
CTCGCTGCCCTTGAGGACAAGCAACTGCCACCACCGTCACTCACGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGATCGGGATGGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLEAAASPLSTPTSAQAAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDLDCSDGSDEEECRIEPCQKGQCPCPCTGVSDCSGGTDKKL
RNCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACACGGTCCGGTCTCGCTCGCGAGCGGCGGAGCAGAGGTGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGAGGAGGAGGAAGGAAGGAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCACACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCGGCATTCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAGGCTCTGTAGCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAAGTGA
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCAA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTGTCAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCAATTGTGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTCCGGTGGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGTCTCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTAGTCACGGAGATTGCT
GCCACCCGGCCTTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCT
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCCTGA
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGGCCACTTCCCCCAGGGGGCTCCCCGGAG
TTCCAGCAGTGACCCCTGACTTGTGGTAGACGGCGTGCCTCATGCTCCGTCTATG
ACGAAGCTGTGAGTGGGGCTTGAGTGCCTTAGGCCCCGGTACATGGCCTCTGTGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTGAGCTGCCAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCACCCCTGCTCGACAAACCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAAAAAATTCCAAAGTGCCTGAAGTGTCTCTCAA
ATACATGTTGATCTGTGGAGTTGATTCCCTTCTCTTGTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTGATCAAGTC
CTGTTCTTCTGACACAGACTGATTAAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPIQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCCCCGCCTCCCGTGCGGTCCGTCGGTGGCCTAGAGA
TGCTGCTGCCGCCGGTTGCAGTTGTCGCGCACGCCCTGCCGCCAGCCCGCTCCACCGCCGT
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAACCGCGCTACAGG
CCGTGCTGCTGCCGTGCTGGTGGGCTGCCGCCGACGGTCGCCTGCTGAGTGCC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAAATGATAGAA
AAGTTCATTGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCCGTGA
GGAGAAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT
CACAATTAGGAACTGGTATGTGGATGAGCCGTCTGCCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACAAATTCATTGCAAATATTCTGATGAGAACCCAGCAGTTCC
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACAGCTGCCTTGAATCTGGCCTACAT
CCTAATCCCCAGCATTCCCCCTCTCCTCCTCCTGTGGTCACCACAGTTGTATGTTGGTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCATC
TGGCCCTCTCCTCACCAGGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTCATTCCGAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAATGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGAACAAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGGACCCCCACGTTGGCTGTATCCTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGCACTTGGTTGGTTGTATCTAACTTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGGCTGTGGAGCTGGAAAACCACCTCTGTTCTGCTCTACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIKEKFIENLLPSDGDFWIGLRRREEQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAALNAYILIPSIPLLLL
VTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFS PDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCTACCACCATGATACTGGTGT
GTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTGTTGACACACGGGCTGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTTGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAAAGTCTGTATCCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAAGTGGACTTCTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAAACCTCCAAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGACTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTTTAATGACCCCTGGGATTTGACCACAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACGTATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVYTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTGCAGCTAAA
ACTAAATATTGCTGCTGGGGACCTCCTCTAGCCT
TAAATTTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTGATCCTT
GCCATTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGC
GGCTGGTGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAA
AGGCCAGTGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCC
GGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAA
AGAGCAAAAGGT
CCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATA
CATTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGA
ACCCAGAGAGCTCTTCTCCCCA
GTCCCAGAGGGTGTCA
GGCTGGCTGACGCCCTGGCATTGCAAGGGAC
GCGTGGAAAGTGAA
GCACCA
GAGAAC
CAGTGGTATACCGTGTGCCAGACAGGCTGGAGC
CTCCGGCCGAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGAGGGCTGTACTGACT
CAAAAACGCTGCAACA
AGCATGCC
TATGGCCGAAA
ACCCATCTGGCTGAGCCAGATGTCATGCTCAGGAC
GAGAAGCAACCCTCA
GGATTGCCCTTCTGGCCTTGGGGAAAGAACAC
CTGCAACC
ATGATGAAGACACGTGGT
CG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACA
ACCTCTGCTCTGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTGTGATGACA
ACTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGCTGTGG
AAGTCCCTCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGCCGCATCTGGCTGGATA
ATGTTGCTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGC
CAGCACAGATT
TTGGGTTTCACGACTGC
ACCCACCA
GAGGAAGA
TGTGGCTGT
CATCTGCTCAGTGTAGGTGGC
ATCATCTAATCTGTTGAGTGCCTGA
ATAGAA
GAAAAACACAGAAGAAGGGAGC
ATTACTGTCTACATGACTGC
CATGGATGA
ACACTGATCT
TCTTCTGCCCTGGACTGGACTTATA
ACTTGGT
GCCCTGATTCTCAGGC
CATCAGACATAGTTG
GAACTACATCA
CCACCTTC
CTATGTCTCCACATTGC
CACACAGCAGATT
CCCAGC
CTCCATAATTGTGT
TAT
CAACTACT
TAAATACATTCT
CACACACACACACACACACACACACACACACACAC
ACCA
CACCATTG
CCTGTTCT
CTGAAGAA
CTGAC
AAAATACAG
ATT
TTGGTACTG
AAAGAGA
TTCTAGAGGAAC
GGA
ATT
TTAAGGATA
AAATT
CTGA
ATT
GGTT
AT
GGGTTCT
GAAATTG
GCTCTATA
AT
CTAATT
AGATA
AAAATT
CTGGTA
ACTT
ATT
ACAATA
ATAAAAG
ATAGC
AC
TATGTGTT
CAAA

FIGURE 54

MALLFSLILAICTRPGLASPSGVRLVGGHLRCEGRVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPDFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGCGTCCCGGGACCGCGTGGGCGGACCGCGTGGGCCGGTACCAAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCTGGG
CGTCTTCGGCCTCTCCGGCTGCTGCAGTGGTGCGCGGGAAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACCAAGTGG
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCAGTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGTCTGCGTGCCGAGATGAAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCAGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCAAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTCCCTGGCTGTTATCTCGAA
CTCTGGCTCCTGGCTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGTCTACAAGTGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAGGGCGGCCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCATGGCCCAACTTGTATTGCAGCTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLQQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI
VAAAELQCFGYVDIL
VNNAGISYRGTIMDTTDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 58

MKFLLDILLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAEGDVSILVNNAGVV
YTSSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCACCGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGGCTC
AGGGAGGAGCACCAGCTGCGCCGCACCCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCTGTTGATGCCTGGCCCTGTGATGGCTGTTCGCTCCCTACAGAACT
GTTCCATGCCACCTAACGGAGACTCAGGACAGCCATTATTCACCCCTACATTGAAGC
TGGGAAGATCCAAAAAGGAAGAGAATTGAGTTGGTCGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTTC
TTCCCAGCTCAGATAACGCCAGAAGATGCCAGTAGTTCTCTGGCTACAGGGTGGCCGGG
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGGCCTTATGTTGTCACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCCTGGACCACAAACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTTATAACAGTGCACTAATTCAAGTTCCAGATATTCCTGAATATAAAAATA
ATGACTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAAATTGCTATTGGAGA
TGGATATTCTGATCCCGAACATTATAGGGGCTATGCAGAAATTCTGTACCAAATTGGCT
TGTTGGATGAGAACGAAAAAAAGTACTTCCAGAACAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCAGCTAAC
AAGTGCACCCCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCCTG
GCACGGAACCTGAGGATCAGCTTACTATGTGAAATTTCCTGCACTCCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACATAGTTGAAACTATAGTTGAAAAGTACTTGC
AGATAACAGTACAGTCAGTTAACGCACTGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAACGGCAGAAAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAAATTATC
GAGGTGGAGGACATATTTACCTATGACCAAGCCTCTGAGAGCTTGACATGATTAATCGA
TTCATTATGGAAAAGGATGGATCCTTATGTTGGATAAAACTACCTTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCAAGGAATAAAAAAA
TTATCTTTCATATGCAAGATTTCATCAATAAAATTATCCTGAAACAAAGTGAGC
TTTGTTTGGGGGAGATGTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGTATAAATGA
AATTTAGGGTCTGAAATAGGAAGTTAATTCTTAAGAGTAAGTGAAAAGTGAGCTT
TAACAAACAAAGCTGTAACATCTTTCTGCCAATAACAGAACGTTGGCATGCCGTGAAGGT
GTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA
TAGTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGRELSL
VGPFPGGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTNSNMTLRDRDFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFEILDKLLDGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKVKWKIFKSDSEVAGYIRO
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGGCTACAACAT
TTTCCCTTCCTAACAGTTCTAACAGCTGTTCAACAGCTAGTGATCAGGGGTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTACCGAGCTCCTT
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCCTGCCTAACAAAGCTTCAAAAAACAGGAGCGACTTCACTGGCTGGGAT
AAGACGTGCCGGTAGGATAGGAAGACTGGGTTAGTCCTAACAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTGTAAAATAAAATTAAAGCAAGTATTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGGGAGAAAGTATGTTAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGAGGGACCCCTGGTC
AGGCCAGCCTTTGCTCCTCCGGAAATTATTGGTCTGACCACTCTGCCTGTGTTT
GCAGAATCATGTGAGGCCAACCGGGAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGG
ACAGCCGCTCTGGTCTGCTCTCAGTGGTCTGGGTGCTGGCCCCCAGCAGCCGGC
ATGCCTCAGTTCAGCACCTCACTCTGAGAACATCGTACTGGACCTCAACCACGTGACCGT
CCACCAAGGGACGGGGCGTCTATGTGGGGCCATCAACCGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAAAGACAGGGCAGAACAGGGACAACAGTCTCGTTACCCG
CCCTCATCGTGCAGCCCTGCAGCGAAGTGCCTCACCAACAAATGTCAACAAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGAGCCTCTACCAGGGGTCTGCA
AGCTGCTGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAAGACGGCACCATGTACGGGTGATTGTGCCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATGGCACGGCTGTGGATGGAAAGCAGGATTACTTCCGACCCCTGTCCA
GCCGGAAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTTCAGACACCCCTGGCCCTGGTCTCCACTTGACAT
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA
CCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATCGTCCGG
CTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGCTCCCTGCCCTCGGCTGCACCCGGGC
CGGGGTGGAATACGCCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGACTCACTGGCCC
AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTGCCATCTTCTCAAAGGGCAGAAG
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGCTACCAAGGGCAGGGCAACCTGGAGCTCAACTGGC
GCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAAGGGCAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCCTGTCCCCATCGATGATAACTCTGTGGA
CTGGACATCAACCAGCCCCTGGAGGCTAACACTCCAGTGGAGGGCTGACCCGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTAGCTATTGGTGGAGATTAACTATAG
ATTACACCTCCTCAGCAAAGAGTCCCTTGGAGGTAGCTATTGGTGGAGATTAACTATAG
GCAACTTATTTCTTGGGAACAAAGGTGAAATGGGAGGTAAGAAGGGTTAATTTGTG
ACTTAGCTTCTAGCTACTCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCACCAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLLSVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTGHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLACGSL
YQGVCKLLRLDDLFLILVEPSHKKEHYLSSVNKTGTMGYGIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPISDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHGSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSAACPIRAINLQIKERLQSCYQGEQN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGGGCTGAGTGC GGACTGGAGTGGAACCCGGGCCCCGCTTAGAGAACACGCGATGACCA
CGTGGAGCCTCCGGCGAGGCCGGCCACGCTGGGACTCCTGCTGGCTCGTCTGGCTCCTGGTGCCTC
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGGATCTTGGGGCTCCATCCACTATTCCTGAGGCTGCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTCTGGATCTTGGGGCTCCATCCACTATTCCTGAGGCTGCAAGGGCTGCAAGGGCTGGA
GGAGGGACCGCCTGCTGAAGATGAAGGCTGTGGCTGAACACCCCTCACCCACTATGTTCCGTGGAACCTGCAAGGGACT
AGCCAGAAAGAGGCAAATTGACTTCTCTGGGAACCTGGACCTGGAGGCTTCGTCTGATGGCCGAGAGATCG
GGCTGTGGGTGATTCTCGTCCAGGCCCTACATCTGCAGTGAGATGGACCTGGGGCTTGCCAGCTGGCTAC
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTACAAGGGCTTCACCGAAGCAGTGGACCTTATTGACC
TGATGTCCAGGGTGGTGCCTACAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATG
GTTCTATAATAAAAGACCCCGATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGGAACTGC
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGATTGTCCAGGGAGTCTTGGCCACCATCAACTTGCAGT
CAACACACGAGCTGCAGCTACTGACCACCTTCTCTCAACGTCCAGGGACTCAGCCAAGATGGTGTGGAGT
ACTGGACGGGGTGGTTGACTCGTGGGGAGGCCCTCACAAATATCTTGGATTCTTGTGAGGTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGGCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTGGCTTCATGAATG
GAGCCATGCACCTCCATGACTACAAGTCAGATGTACCAGCTATGACTATGATGCTGTGACAGAACGGCG
ATTACACGCCAAGTACATGAAGCTCGAGACTTCTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCCACCTG
ACCTTCTTCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTGTACCTGTCTGTGGACGCCCTCAAGTACC
TGGGGGAGCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGAAATGGACAGTCCT
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCACGTGCATGATGGGGCAGG
TGTGTTGAAACACAGTATCCATAGGATTCTTGGACTACAAGACAAGAACGATTGCTGTCCCCCTGATCCAGGGTT
ACACCGTGTGAGGATCTTGGTGGAGAACGTCAGTGGGAGTCAACTATGGGGAGAATATTGATGACCAGCGCAAAG
GCTTAATTGAAATCTCTATCTGAATGATTCAACCTGAAAACACTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTCAGAGGTTGCCCTGGACAAATGGNGTCCCTCCAGAAACACCCACATTACCTGCTTCTTCTTGG
GTAGCTTGTCCATCAGCTCCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGAGAACGGGTTGTATTCA
TCAATGCCAGAACCTTGGACGTTACTGGAACATTGGACCCAGAACAGCAGCTTACCTCCAGGTCCCTGGTTGA
GCAGCGGAATCAACCAGGTATCGTTTGAGGAGACGATGGGGCCCTGCATTACAGTTACGGAAACCCCC
ACCTGGGCAGGAACCAAGTACATTAAAGTGAGCGGTGGCACCCCTCCTGCTGGTGCAGTGGGAGACTGCCGCCTC
CTCTTGACCTGAAGCCTGGTGGCTGCTGCCCAACCCCTCACTGCAAACAGCATCTCCTTAAGTAGCAACCTCAGGG
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTCAAACCTAAGCCTGCAGGGAAAGGTGGATGGCTCTGGGCC
TGGCTTGTGATGATGGCTTCTACAGCCCTGCTCTTGCTGCCAGGCTGTGGCTGTCTAGGGTGGAGC
AGCTAATCAGATGCCAGCCTTGGCCCTCAGAAAAGTGTGAAACGTGCCCTGCACCGGACGTACAGCCC
TGCAGCATGCTGGACTCAGCGTGCTTTGCTGGTTCTGGAGGCTGGCCACATCCCTCATGGCCCCAT
TTTATCCCCGAAATCCTGGGTGTGTCACCAGTGTAGAGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCCTTACAACCTTCTGAGCCTTGGGATTCTGGAAGGAACCTGGCGTGAGAACATGTGACTTCCCTT
TCCCTTCCACTCGCTGCTTCCACAGGGTGACAGGCTGGCTGGAGAAACAGAAATCCTCACCGTCTTCC
CAAGTTAGCAGGTGTCTGGTTCAGTGAGGAGGACATGTGAGTCTGGCAGAACGCATGGCCATGTCTGCA
CATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCATGGCCATGTCTGCA
AGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCATGGCCATGTCTGCA
GGAGGAGAACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCATGGCCATGTCTGCA
ACAGAACGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCCAGCCCCAACAGCAGGGCAGAGCAGGCCCTC
GAAGTGTGTCAGTCCGCTTGAACCTGGCTTCTGGGCCCAGCCAAACACCTGGCTTGGCTACTGTCTG
GTTGCAGTAAAGCTATAACCTGAATCACAA

FIGURE 64

MTTWSLRRR PARTLGLLLL VVLGFLVLRRL DWSTLVPLRLRHRQLGLQAKGWNFM LEDSTFW
IFGGSIH YFRVPREYWRDRLLKMKACGLNTLTTYVPWNLHEPERGKFDFSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFT EAVDLYFDHLMMSRVVPLQ
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSNDG LSKGIVQGVLAT
INLQSTHELQLLTTFLFNVQGTQPKMVMEYWTGWFDSWGGPHNILD SSEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKL RDFFGSISGIP
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSF GYI LY
TSITSSGILSGHVHDRGQVFVNTVSIGFLDYKTTKIAVPLI QGYTVLRILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSP LKNFRIYS LDMKKSFFQRFGLDKWXSLPETPTLPAFFLGSL SIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGTGGACGGGCCCCAGGAC
CTGGTGAGGGTTCTACTTGGCCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGCTCGGCCCGAGGCCCGAGGACCTCCATCTCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
AAGAAGCTGTCCTGCCTCGTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGTCGTTAGTGGATAGGGGTATGACCGGTTCTCCTAGACGGGCCC
CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTCGGTACCGCGGGTGTGCTTGGGCCAC
CGGCTTTGAAGATGCGATGGAGCGGCCTAACGCCATACAGTTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA
ATGAGGCAGCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCCATCCTGGTCTCGAAAACCTGAAATTCAAGAACCTC
AGATCCAGACTTCCTGCCGCAGTGGACTCCTGGTTCAAGGTCTGCTGCCCAAGATATATC
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGCTCTCCGTGCAGCTGCTAGG
AGAAAAGATCTTGCTCTCACACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GAACCTACCAACTGTAGATTGGCCAGCTGACAACATGACCAAAATCTTACCCCTGCTT
CGGAAGTATGAACCCCATTGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGCCAGAACATCACTCCACACGGCTGTGTCAGCTGTAACCAAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCCTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGACCCCACACCTAACGCTTTGCTCTCGAGATGTCAAGT
TCCAGGAAGTTCTGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGT
ACTCTGCACCTGGTGGCATTACTGGCTTCAGACTGCTTGGCTGGCCCAT
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGTGCCAAATAATGGAGTC
CATGACCGTGCCTATGTGATGGTGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG
AGACAAACTATTGGACGGGAAACTGGGTCCAAACTGGATATCTTGGTGGAGAACATGG
GGAGGCTCAGCTTGGGTCTAACAGCAGTGACTCAAGGGCCTGTTGAAGCCACCAATTCTG
GGCAAACAATCCTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCTCCAGTGTGCCAAATGGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTAACCTGGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCCTACGTGCCAAGATTCCCTGCTGTTCCAGGGAGCCCTCAACAAAATTA
CATTGCTGGAACTAGAAGATGTACCTCTCAGCCCCAAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATAACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGGCACTGTGAAAGGTAGGCCGGCATGGTGGCTCATGC
CTGTAATCCCAGCACTTGGGAGGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCCAACATGGTGAACACCCGTCTCCACTAAAAATACAAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGGCTGAGGGCAGGAGAATTGCTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFSYMRHLAGLFRAALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRVSATKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPPLGPLPPSPKMM
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMHTIFEPTFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSAEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGC
ACCCACAATATGGCTTACATGTTAAAAAGCTTCTCATCAGTTACATATCCATTATTCAGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAGGATACCTTGAAGGAATATT
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAAACGATT
GCGTTCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGTTAGTGAAAATAACTTAGGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGA
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCATTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGTGTATTGCTCAAAA
CCTTCGAGAGTTGACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCAATTACAGGA
ACTGGATTTAAAGTCCAATAACATTGCAACATTGAGGAAATCATCAGTTCCAGCATT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCTATTACCCATGTCA
AAAACCTGGAGTCACTTATTCTCTAACAAACAAGCTCGAACCTTAC
AGCTGGCAGTATTAGTTACAGATGCTTAGATGTGAGCTACAACAA
ACTGGACATTCAATGATTCCAAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTGATAACCCTGCCACTCGAAGTCAAAGAGGGATTGAATCAAGACATA
AATATTCCCTTGCAAATGGGATTAAAACTAAGATAATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATT
AGTAGTGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTAAGGGTTTAAGTCATTCAATTCAAATCATT
TTTTTTTTCTTTGGGG
AAAGGGAAAGGAAAAATTATAACTAAATCTTGGTTCTTTAAATTGTTGTAAC
GCTGCCGCTACTGAATGTTACAAATTGCTGCCTGCTAAAGTAA
ATGATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDF AFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRHISRNAQDKQELHLFMLSG
VPDAVFDLTDLDVLKLELIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKLNRELYLIGNLNSENNKMICLGELESLRELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAEELQNCERIPHAIFSLSNLQELDLKS
NNIRTIEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCLDRLPAQLGQCRLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACCGCGTCCGGCCTCTCTGGACTTGCATTCCATTGACAAACTGACTTTTATTCT
TTTTTCCATCTCTGGGCCAGCTGGATCCTAGGCCGCCGGAAAGACATTGTGTTTACACACATAAGGAT
CTGTGTTGGGTTCTTCTCCTCCCCTGACATTGCATTGCTAGTGGTGTGGGGAGGGAGACCACGTGG
GCTCAGTGCCTGCTTGCACTTATCTGCCTAGGTACATCGAAGTCTTGACCTCCATACAGTGATTATGCCIGTC
ATCGCTGGTGGTATCCTGGCGGCCCTGCTCTGCTGATAGTGTGCTGTCTTACTCAAAATACACAAAC
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGAAAAAATACAACCCAGACAAGGTGTGGGGCCAAG
AACAGCCAGGCCAAAACCATTGCCACGGAGTCTTGTGCGCCCTGCAGTGTGAAGGAATAGAATGTGTGCC
AGTTTGATTCCCTGCCACCTTGCTGTTGCGACATAATGAGGGCCTTGAGTTAGGAAAGGCTCCCTCTCAAA
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTGTGATGTGCGAGCACAGAAGAAAGGCACAG
CTCCCCATCAGTTCATGGAAAATAACTCAGTGCCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGCAACCCCTCCAGGAAGGAGTTGGGGAGAGAGAACCTCACTGTGGGAATGCTGATAAACAGTC
CACAGCTGCTCTATTCTCACACAAATCTACCCCTGCGTGGACTGACGTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCCTATAAAAGCTGCGGTCTTAAGGCTGCCAGCGCCTGCCAAAATGGAGCTTGT
AGAAGGCTCATGCCATTGACCCCTTAATTCTCTCCTGTTGGAGCTGACAATGGCGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGTGCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGACAGAAAACAAAGCATCAGAATTATCTTCTATGTCCAGCTT
GATCCAGATGGAAGCTGTGAAAGTAAAAACATTAAAGTCTTGACGGAACCTCCAGCAATGGCCTCTGCTAGGG
CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTGAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GAUTCAGCAAGAATTCAAAGAACTGTCTTGTCTTACTACTTCTCTCCTAACATCTTCTATTCCAAACTGT
GGCGTTACCTGGATACCTTGAAGGATCCTCACAGCCCCAATTACCCAAAGCCGATCCTGAGCTGGTTAT
TGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAAACTCAAAGAGATTTCCTAGAAAATAGAC
AAACAGTGCAAATTGATTTCTGCCATCTATGATGGCCCTCCACCAACTCTGGCTGATTGGACAAGTCTGT
GGCCGTGTGACTCCCACCTCGAATCGTCATCAAACCTCTGACTGTCGTGTCTACAGATTATGCCAATTCT
TACCGGGGATTTCTGCTTCTACACCTCAATTATGCAGAAAACATCAACACTACATCTTAACCTGCTCTTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTAACTCTAATGGGAAATAACTGCAACTAAA
GACCCAACTTGCAGACCAAAATTATCAAATGTTGGAATTTCCTGTCCTCTTAATGGATGTGGTACAATCAGA
AAGGTAGAAGATCAGTCATTACTACACCAATATAACCTACCTTCTGCATCCTCAACTCTGAAGTGATCACC
CGTCAGAAACAACCTCAGATTATGTAAGTGTGAAATGGACATAATTCTACAGTGGAGATAATATAACATAACA
GAAGATGATGTAATACAAAGTCAAATGCACGGGCAAATAACACCCAGCATGGCTCTTTGAATCCAATTCA
TTTGAAGACTATACTGAATCACCATTATGTTGAAACCAAACCTTTGTTCAAGTTAGTCTGCAC
ACCTCAGATCCAAATTGGTGGTCTTGATACCTGTAGAGCCTCTCCACCTCTGACTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTGTAAGGTGTATCCCTTATTGGACACTATGGGAGA
TTCCAGTTAATGCCCTTAAATTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAAGTTGATATGTGAT
AGCAGTGACCAACCAAGCTCGCTGCAATCAAGGTTGTCTCCAGAAGCAAACGAGACATTCTCATATAAATGG
AAAACAGATTCCATCATGGACCCATTGTCGAAAGGGATCGAAGTGCAGTGGCAATTCAAGGATTTCAGCAT
GAAACACATGCCGAAGAAACTCCAAACCCAGCCTTCAACAGTGTGCATCTGTTCTCATGGTTCTAGCTCTG
AATGTGGTGACTGTAGCGACAATCACAGTGAGGCATTGTAATCAACGGGCAGACTACAAATACCAAGACTG
CAGAACTATTAACTAACAGGTCCAACCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTATGAATAATGAGGAAGGGCCTGAAAGTGACACACAGGCCATGTAAAAAAA

FIGURE 70

MELVRRLMPLTLLLILSCLAEALTMAEAEGNASCTVSLGGANMAETHKAMIQLQNPSENCTWTI
ERPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLGVCSKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDITLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSIYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLIQDSSDHQSRCNQGCVRSKRDIISSYKWKTDSIIGPIRLKRDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGC
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCCACGCCAGCGCTCGACCCACCTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGTGGTTGACCAGGCAAGTCGGCATCTCATCCACTG
GGGAGTGTTCAGCTCGGTAGCGAGTGGTCTGGTGGTATTGGCAAAAGGAAA
AGATAACCGAAGTATGTGGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT
TTTGGACCACTATTTACAGCAAAATTTTAATGCCAACAGTGGCAGATATTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACCTCCAAACATCATGAAGGCTTACCTGTGGGGGT
CAGAATATTGTGGAACGTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA
ATGGTTTCACTCGCTTCTGAGGATGAATCCAGTTCACTCCATAAGCGCAATTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTTGGCCTGGTT
ATATAATGAAAGCCCAGTTGGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTCTACCTGCAGTGATCGTTATAACCCAGGACATCTTGCCA
CATAAATGGGAAAATGCATGACAATAGACAACTGTCCTGGGCTATAGGAGGAAAGCTGG
AATCTCTGACTATCTACAATTGAAGAATTGGTAGAAGCAACTTGTAGAGACAGTTCATGTG
GAGGAAATCTTTGATGAATATTGGGCCACACTAGATGGCACCATTCTGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGTCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTCTAAATGGCCACATCAGGACAGCTGTCCTGGCCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC
GATTCTTGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATCAGATGC
CGTGTAAATGGGCTGGCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAAACTGGATAAGAAAATTATTGGCAGTTCAGCCCTTCCCTTTCCACTA
AATTCTTCTAAATTACCCATGTAACCATTAACTCTCAGTGCACCTTGCCTTAAAGTC
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTATGTTGAAGCCATATCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTAGGTAGACTGTTGCTCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGTAAAATAATGGTGCACCTGTATAGGGCACTTACCAAGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAAATACTGTATGCTTAGGCTACACTACATTATAAAAAAA
GTTTTCTTCTCAATTATAAATTAAACATAAGTGTACTGTAACTTACAAACGTTTAATT
TTTAAAACCTTTGGCTTTGTAATAACACTTAGCTAAACATAAAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEFWWYWQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETY
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACG**ATGGCCAGGTGCTTCAGCCTGGTGTG**
CTTCTCACTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTGCAGCAGAAGAGCT
TTCCATCCAGGTGTCACTGCAGAATTATGGGGATCACCCCTGTGAGCAAAAAGGCGAACCGC
AGCTGAATTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAACACTTGAGCTATGGCTGGTTGGAGA
TGGATTCGTGGTCATCTCTAGGATTAGCCAAACCCAAAGTGTGGAAAAATGGGGTGGGTG
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACATCTGAT
ACTTGGACTAACCGTGCATTCCAGAAATTATCACCAACAAAGATCCCATATTCAACACTCA
AACTGCAACACAAACAAACAGAATTATTGTCACTGACAGTACCTACTCGGTGGCATCCCC
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTACAGAAGTTTATGGAAACTAGCACCAGTCTACAGAAC
TGAACCATTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGCAGCTGGTCTGGATTTC
TATGTCAAAAGGTATGTGAAGGCCTCCCTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCATGATAGCAACCTAATGAGGAATCAAAGA
AAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAA
GCTGAAGTT**TAG**ATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCACTGCTCC
TTACCCCTGCCCTAGCTGGGAAATCAAAAGGCCAAAGAACCAAAGAACAGTCCACCC
GGTTCTTAACGGAAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC
CCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC
TTTCTAGCCTGGCTATGCTTAATAATATCCCACGGAGAACAGGAGTTTGCAAAAGTGC
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCCTGGCTGTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCAGTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC
CCTTCTCAGCTCTGAAAGAGAACACGTATCCCACCTGACATGCTCTTGAGGCCGGTA
AGAGCAAAGAACGGAGAAAGCTTACGGCTGGGAAAGCCATGGAGATTCTCATAACTGAG
ACCTAATCTCTGTAAGCTAAAGCTAAAGAACAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTCT
AGGAAATATACTTTACAAGTAACAAAAAAACTCTTATAAATTCTATTCTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTCT
GTTTGATATTCTAGCTTACTCTCAAAACTAATTGTTATTGCTGAGACTAATCT
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTACATACCTAAGAAC
TACATTGTTACCTCTATATACCAAAAGCACATTAAAAGTGCCATTAACAAATGTACT
GCCCTCCTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATTGTGACAAAAAATTAA
AGCATTAGAAAATT

FIGURE 74

MARCFSLVLLTSIWTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNSPKCGKNGVGVLIWKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDFNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTGGCACCTCTAATTGCTCTCGTGTATCGGTGCCGCGACTTACGATGG
CTCGCCCAACCTTACTACCTTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACCTAGAACGGGACAAGAGGGTCACGGATTGTGGAGTTCTTGCAA
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGGAAGGTGGATGTTGGACGCTACTGATGTTAGTACGGTAC
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTCTG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTTCAACCCCCACCACAGTGTAGA
TGGGGAAAACAAGAAGGATAAATAAGATCCTCACTTGGCAGTGCTTCCTCCTGTCAATT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTCCCTTGG
CTGNGACTGGNTGGGCAGCATGCAGCTTGATTTAAAGAGGCATCTAGGAAATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGTGGTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGAAATGGTTCCCTCCAAGCTTGGTCAGTGTGTTACTGCTTATC
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTTCTTAG
TTGACCTGCACAGCTGGTAGACCTAGATTAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTCCCCCAAGGACTCTGCTTCCCTAAGCCCTCTGGCTCGTTATGGTC
TTCATTAAAAGTATAAGCCTAACTTGTGCTAGTCCTAAGGAGAAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTGTGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGGTAGGACTTGGAGGAGAAACCCCTGGACTTCAC
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSPVRLSRWLAQPYYLLSALLSAAFLVRKLPPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGGGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGACGTTGCCCTG
GGGCCCCAGCCTGGCCGGGTACCCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCA
TTGCTCCTGCTGCCGGCTCCTACGGACTGCCCTCTACAACGGTTCTACTACTCCAACAG
GCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCCTGTTCACCTACCAAGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGGCGTGTGCGTGTCAAATGGTGGAAAGCT
GTCGGAGAACGGGGCCCCAGAGAACGGACGTGCTGGTGGCCATGGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCCGTGCACCTGCCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCCGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCCGGGTGTGGCTTCTTACCAAGTCCCCCA
ACGGCGCTACCAGTTCAACTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCCGTG
GTGGCCTCTTGAGCAGCTCTCCGGGCCTGGAGGAGGGCCTGGACTGGTGCAACGCCGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGCAGCCCTGCCGTGGCC
CAGGCCTGGCACCTGGCGTGCAGACTACGGCCCCGCCACGCCGCCTGCACCGCTATGAT
GTATTCTGCTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAACGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC
AGCTCTTGCCGCCTGGAAGTTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCCTGTGGTTACCCGCATCCTAACTGTGGGCCAGAGCCTGGGGT
CCGAAGCTTGGCTTCCCCGACCCGCAGAGCCGCTGTACGGTGTACTGCTACCGCCAGC
ACTAGGACCTGGGGCCCTCCCCCTGCCGCATTCCCTCACTGGCTGTATTATTGAGTGGTT
CGTTTCCCTGTGGGTGGAGCCATTAACTGTTTATACTCTCAATTAAATTCT
TTAACATTTTACTATTTTGAAAGCAAACAGAACCCAAATGCCCTCCCTTGCTCCTG
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGGCATTGCGGTTTGCTGGCTCTG
GAGGGTTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGGCCAGAGTGGC
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGGCATGGTGGCACAGTTCTCCCTGCC
CAGCCTGGGGGAAGAACAGAGGGCCTGGGGCCTCCGGAGCTGGCTTGGCCTCTCCTGCC
CACCTCTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTCCAGGCAGGAAATCTGAGGGAAAGGAAGAAACTCCCTCCCCGTTCC
TCCCTCTCGGTTCAAAGAACATCTGTTGTCATTGTTCTCCTGTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGTATGACTGCCCTCCGCCAA
AA
AA

FIGURE 78

MGLLLVPLLLPGSYGLFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEELDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCGGCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAA
CTTCCAGTACGACCATGAGGCTTCCTGGGACGGGAAGTGGCCAAGGAATTGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGTCTGGGGCGATCGTGGACCGCATGGACCGCGCGGGGAC
GGCGACGGCTGGGTGTCGCTGGCCGAGCTCGCGCGTGGATCGCGCACACGCAGCAGCGA
CATACGGACTCGGTGAGCGCGGCCTGGGACACGTACGACACGGACCGCGACGGCGTGTGG
GTTGGAGGAGCTGCGAACGCCACCTATGCCACTACCGCCCGGTGAAGAATTGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTGGGACGAGCGCGTTCCGGGTGGC
CGACCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTCCTGCACCCGAGG
AGTTCCCTCACATGCGGGACATCGTGTGATTGCTGAAACCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCCGGACTTCCGGATCTGAACAAAGG
ATGGGCACCTGGATGGAGTGAGGTGGCCACTGGGTGCTGCCCTGCCAGGACAGCCC
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGTGAGCAA
AGCGGAAATCCTGGTAATTGGAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACACGATGAGTGAGCACCAGCACCTGCCACAGCCTCAGAGGCCCG
CACAAATGACCGGAGGAGGGCCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCGCAGGAG
GCAGATGCAGTCCCAGGCATCCTCCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC
TGTCCCTGTCACACCCCCAACCCCAAGGGAGGGCTGTCAAGTCCCAGAGGATAAGCAATAC
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCATAGACTGAAACTCCCCT
GGCCCCAGCCCTCTCCTGCCTGGCCTGGACACCTCCTCTGCCAGGGAGGAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKDGHLDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTCCGCACTCGGGCGCAGCCGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGGCGCGGGTGCAGGGATCCCTGACGCCTCTGTCCCTGTTCTTGTGCGCTCCAG
CCTGTCTGTCGTCGTTGGCGCCCCGCTCCCCGCGGTGCGGGTTGCACACCGATCCTG
GGCTCGCTCGATTGCCGCGAGGCGCCTCCCAGACCTAGAGGGCGCTGGCCTGGAGCAG
CGGGTCGTCTGTGTCCTCTCCTCTGCGCCGCCGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACGCCGGGCTCCGCACCCCTGCCCTGCCCTGCCCCATTCTCCCTCTCCCAG
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCGGCTCTGCCCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGCCGCCGGCAGCGAGGGAGCCGCTCCATTGCTATCACATG
TTTACCAAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCCTGCCCCAGGGGCTGCC
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTAGCCTACC
TGGTCGAGAAAACATTCCCTCAGTAGATGCCATGGCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTTCTTCACAGTAACAAAGGAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCGAGAAGAAAACGG
CAATAAAGATTGTAAAGCAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGGCAGC
GCCGATTAAATTACAGAAGAATTGTTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTACTTGAA
AAACTTACATCAGCCAAAGATGTTGTTGCCATAAAGGAAGTAGGTTCAGAGGGGTA
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTATTGATGGTGGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTCTTACACATGCCAACTGGTTGGCACCACAAAATACGTAAA
GCCTCTGGTACAGAACAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTAACT
CAGTGAACATTGCCTTCTAATTGATGGCTCCAGCAGTGGAGATAGCAATTCCGCCTC
ATGCTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCCAAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA
AAGAGAATGTCCTAGCTGTCACTAGAAACATCCGCTATATGAGTGGGAACAGCTACTGGT
GATGCCATTCCCTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCTAGTAATTGTCACAGATGGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCACTATCTCTGTTGGTGTGGCTGGCACCTCTGGATGACCTG
AAAGATATGGCTCTAAACCGAAGGAGTCTCACGCTTCTTACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCACTCAGAGGCATTGTTAGAGATTCTTAGAATCCCAGCAAT
AATGGTAACATTGACAACTGAAAGAAAAAGTACAAGGGATCCAGTGTAAATTGTATT
CTCATAACTGAAATGCTTACTGCTACTAGAACATCAGATACAAAATTAAGTATGTCAAC
AGCCATTTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTTTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAA

FIGURE 82

MSAAWIPALGLVCLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVY
GNIVYASVSSICGAAVHRGVISSNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRLMLEFVSNIAKTFeISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCGCGCTCCCGACCCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGAGCCC
GGCGGCCTCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG
GGGCGGCGGCTGCGGGCGCAGAGGGGAGATGCAGCGGCTGGGGCACCCCTGCTGTGCCTGC
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCGGCCCGGCTCTCAGCTACCCGAGGAGGAGGACCCCTCAATGAGATGTTCCCGA
GGTTGAGGAACTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCAGCTAT
CACAATGAGACCAACACAGACACGAAGGTGGAATAATACCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTACTGCCAGTTGCCAGCTCCAGTACACCTGCCAGCCATGCCGGGGCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCAGTGGAGACCAGCTGTGTCTGGGGTCACTGCACCAAAA
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCCTCCAGAGAGGGCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA
GCTTGCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTGGACCGATGCCCTTGCCAGTGGCCTCCTGTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTCGTGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGATTGGCAGCTCATGGAGGAGGTGCCAGGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGTGCCGGCT
GCACTGCTGGAGGGAAAGAGATTTAGATCTGGACCCAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCCCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTTACCA
TCTTCTTCCAGTAAGTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTTCA
TCCCCCAGGCTGTTCTCCAGGCTCACAGTCTGGCTGGAGAGTCAGGCAGGGTTAAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCCTTACCA
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTCTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAAACATCAA
CCTGGCAAAATGCAACAAATGAATTTCACGCAGTTCTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGAGATGAAATGTTCTGTTCACCTGCATTACATGTGTTATTCA
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCA
CCTCTCTCAGCACGCCTGGGGAGGGGTATTGTTCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCA
CTGGTTGTGACTCTAAGCTAGTGTCTCTCCACTACCCACACCAGCCTGGTGCCACCAA
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTCTTGAGGCATGCACATCTGGAATTAAAG
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGCAGCCGTCTTAATGAAGACAATGATATTGACACTGTCCCTCTGGCAGT
TGCATTAGTAACATTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTGCAAACACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTCACTCCAGAGTTCTAAAGTTAAAGTTGCACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGC
ATAAAACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSVEEEMEAEEAAKASSEVNLANLPPSYHNETNTDTKGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRLMLCTRSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVQLEDLERSLTEEMALGEPAAAAAALLGEEI

Signal sequence:
amino acids 1-19

N-glycosylation site.
amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.
amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.
amino acids 202-208, 217-223

Amidation site.
amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGGAAAGAGGTAAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTCAAGCCCCTCCACTCTCCTCCCTCCAAACACACATGTGCATGTACACACACACATACA
CACACATACACCTCCTCTCCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGGTCAAGAAAAGGACAC
TAAAGCCTTAAGGCAGGGCTGGCATTACCTCTGCAGCTCCTTGGCTTGAGTCAGGAAACATGGGAGGG
CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTGGGAGACCGAGGTGAGCAGATCACTGAGGTCAAGGAG
TTCGAGACCAGCCTGGCAACATGGAGAAACCCCCATCTCTACTAAAAACACACACACACAC
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAATCGCTGAATCCAGGAGGGAGGATGCAGT
CAGCTGAGTGACCGCTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACACACGGGAGGA
GGGGTAGATACTGCTCTGCAACCTCCTTAACCTGCATCCTCTCCAGGGCTGCCCTGATGGGGCCTG
GCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGACGCCG
GTGAGAATGACTGCCCTGGGAGGGTGGTCTTGGGCCCTGGCAGGGTGTGACCCCTACCCCTGCAAAACACA
AAGAGCAGGACTCCAGACTCTCCTGTAATGGTCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC
ACTCTGCTAGCTTGGGTGGCTGGTGCCTGCACACTGTGCCACTGTGCCGTGGTACCCCTGGCATGTTCCCTGCC
GTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCGCTCGCCTACCGCGAGGCTACCAACTGTGGACTGCAATGA
CCTATTCCCTGACGGCAGTCCCCCGGCACTCCCCGAGGACACAGACCCCTGCTCCTGCAGAGCAACAGCATTGT
CCGTGTGGACCAGAGTGAGCTGGCTACCTGGCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTGG
TGCCCGAGACTGTGATTCCATGCCCTGCCAGCTGCTGAGCCTGACCTAGAGGAGAACAGCTGACCCGGCT
GGAGGACACAGCTTGCAGGGCTGGCCAGCCTACAGGAACCTCTCAACCCACAACCAGCTTACCGCATCGC
CCCCAGGGCTTTCTGGCCTCAGCAACTTGCTGCCACCTCAACTCCAACTCCCTGAGGGCATTGACAG
CCGCTGGTTGAAATGCTGCCAACCTGGAGATACTCATGATTGGGGCAACAAAGGTAGATGCCATCTGGACAT
GAACCTCCGGCCCTGGCCAACCTGCGTAGCCTGGTCTAGCAGGCATGAACCTGCGGGAGATCTCCGACTATGC
CCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCCTCTATGACAACACCAGCTGGCCCGGGTGCCAGGGGGCACT
GGAACAGGTGCCCAGGCTCAAGTTCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGACTTGC
CAACATGCTGCACCTTAAGGAGCTGGACTGAACACATGGAGGAGCTGGTCTCCATGACAAGTTGCCCTGG
GAACCTCCCCGAGCTGACCAAGGCTGGACATACCAATAACCCACGGCTGTCCCTCATCCACCCCCGCGC
CCACCTGCCAGATGGAGACCCCTATGCTCAACAACACGCTCTCAGTGCCTGCACAGCAGACGGTGGAGTC
CCTGCCAACCTGCAAGGAGGTAGGTCTCCACGGCAACCCATCCGCTGTGACTGTGTCATCCGCTGG
CACGGGCACCCGTCCGCTCATCGAGCCGAATCCACCCGTGTGCGGAGCCTCCAGCGCCTCCC
GGTCCGTGAGGTGCCCTCCGGAGATGACGGACACTGTTGCCCTCATCTCCCCACGAAGCTCCCCCAAG
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTCTGCATTGCCGGCACTGGCGAACCGAACCGAGATCTACTG
GGTCACTCCAGCTGGCTTCGACTGACACCTGCCATGCAGGCAGGAGGTACCGGGTAGGGCCAC
GGAGCTGCGGAGGGTGACAGCAGAACAGGAGGCTATAACACCTGTGTGGCCAGAACCTGGGGCTGACAC
TAAGACGGTTAGTGTGGTTGTGGCCGTGCTCTCCAGCCAGGCAGGGACGAAGGACAGGGGCTGGAGCTCCG
GGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTGGGTACCCCAACACAGTGTCCACCAACCTCAC
CTGGTCCAGTGCCTCCCTCCGGGCCAGGGGGCACAGCTCTGGCCCTGCCTCGGGAACCCACAGCTA
CAACATTACCCGCTCCTCAGGCCACGGAGTACTGGCCTGCAGTGGCTTGTGATGCCACACCCA
GTTGGCTTGTATGGGCCAGGACAAAGAGGCCACTTCTGCCACAGAGCCTTAGGGGATGTCCTGGCTCAT
TGCCATCCTGGCTTCGCTGTCCTCTGGCAGCTGGCTAGCGGCCACCTGGCACAGGCCAACCCAGGAA
GGGTGTGGGTGGGAGGGCGCTCTCCAGCCTGGCTTCTGGGGCTGGAGTGCCCTCTGTCCGGTTGT
GTCTGCTCCCTCGTCCCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAACAGGGAGACACTGTTGCC
ACCATTGTCTAAATTCTTGAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTACCAA
AGAGAACAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGCCTGGCAGCTGGC
CAAGACAGATGGGGCTTGTGGCCCTGGGGTGCTCTGCAGCCTGAAAAAGTTGCCCTACCTCCTAGGGTCA
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGAGGGACTTGGCTAGAGCCTCCTGCCTCCCCATCT
CTCTGCCAGAGGCTCTGGCTGGCTTGGCTTGGCTACCTGTGTCCCCGGCTGCACCCCTCCTCT
TCTTCTCTGTACAGTCTCAGTTGCTCTGTGCTCTGGCAAGGGCTGAAGGAGGCCACTCCATCTCAC
CTCGGGGGCTGCCCTCAATGTGGAGTGACCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAA
CGCCTCATCTCAGCAGCCTGGCTCGGCATTCCGAAGCTGACTTCTATAGGAATTGTACCTTGTGGAGAA
ATGTGTACCTCCCCAACCGATTCACTCTTCTCCTGTTGTAAAAAATAAAATAATAACAATAAAA
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDSQNSFSDARCDFHALPQLLSSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMMFRPLANLRSVLVAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGLKFLLDNKNPLQRVPGDFANMLHLKELGLNNMEELVISIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHHPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGADTKTVSVVGRALLQPGRDEQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLAAHLGTGQPRKGVGRRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGCCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGAGGGGACATTGTGTACCGCCT
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCAACCC
CCTGGCCACACTCTTCAAGATCCTGGCGTCCCTACATCAGCCTAGTCATCTCTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCGTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTCATGCTGCACCTCATTGACCAATACGACCCGCTACTCCAA
GCGCTTCGCCGTCTCCTGCGGAGGTGAGTGAGAACACAAGCTGCCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGGCTACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGAGCTGATCCCCGACGTGACCATCCCCGCC
CAGCATTGCCAGCTCACGGCCTCAAGGAGCTGTGGCTCTACACACAGCGGCCAAGATTGAAGCGCCTGCC
GGCCTTCCTGCGCAGAACCTGCCAGCTGCACATCAAGTCACCGACATCAAGGAGATCCCCGCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGCAACCTGAGCGCGGAGAACAAACCGCTACATCGTCATCGA
CGGGCTGCCGGAGCTCAAACGCCCTCAAGGTGCTGCCGCTCAAGAGAACCTAAGCAAGCTGCCACAGGTGGTCAC
AGATGTGGCGTGCACCTGAGAACGACTGTCCATCAACAATGAGGGCACCAAGCTCATCGCCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCACCTGGAGCGCATCCCCACTCCATTTAGCCT
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAAACCTCAAGGACCATCGAGGAGATCATAGCTTCAGCACCT
GCACCGCCTCACCTGCCCTAACGCTGAGGAGATCGAGAACGATCCCCACCCAGCTCTACTGCCGCAAGCTGCG
CTACCTGGACCTCAGCCACAAACCTGACCTTCCCTGCCGACATCGCCTCCTGCAGAACCTCCAGAACCT
AGCCATCACGGCCAACGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGCCGAAGCTGCCGGCTGCACCT
GGGCAACACGTGCTGCAGTCAGTCACTGCCCTCCAGGGTGGCGAGCTGACCAACCTGACGAGATCGAGCTGCCGG
CAACCGGCTGGAGTGCGCTGCGTGGAGCTGGCGAGTGCCACTGCTCAAGCGCAGCGCTGGAGGAGCTGGAGGAG
GGACACTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCTGAGCGAG
GCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCCAGGCCGGAGGGCAGGCCTAGCTCTCCAG
AACTCCGGACAGCCAGGACAGCCTCGCGGCTGGCAGGAGCCTGGGCGCTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGGGGCTGCCCTTCTCCCTGAGACTCACGCCCCAGGGCAAGTGCTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGTCTCCCTGGAGGGCAGCTGCCCCAGGGCTGAG
CTGCCACCAGGGTCTGGGACCCCTCACTTAGTTGGTATTATTTCTCCATCTCCACCTCCTCATCC
AGATAACTTACATTCCAAGAAAGTTCAAGCCCAGATGGAAGGTGTTAGGGAAAGGTGGCTGCCCTTCCCC
TTGTCTTATTAGCGATGCCGCCGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGCCGGCGAACCCAG
CCATGGGACGGTCACCCAGCAGTGCCTGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCCCTCAGCTGGA
AAGGCCAGGCCGGCTTGGAGCTTCAGTTGGCAGTTAGTTAGTTGGTTTTTTTTTTTTAAATCAA
AAACAATTTTTAAAAAGCTTGGAAAATGGATGGTTGGTATTAAAAAGAAAAAAACTAAAAAA
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTGAGCAAAGCAGGCCAGACGT
TGAACGTGTTCTTCCCTGGGAGGGAGGTTTTGGTTGGTTGGGTTTTGGTGTCTGGTCTTCTTCTCC
CTATTGTTCTGGGAGGGAGGTTTTGGTTGGTTGGGTTTTGGTGTCTGGTCTTCTTCTCC
ATGTGTCTTGGCAGGCACTCATTCTGTGGCTGTCGGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTTGGCTAATCCCCGGATGAAACGGTGTCCATTGCCACCTCCCTCGTGCCTGCCCTGCCCTCCA
CGCACAGTGTTAAGGAGCCAAGAGGGAGCCACTTCGCCAGACTTGGTTCCACCTCCCTGCCATGGGTGT
CCAGTGCCACCGCTGCCCTCGCTGTTCCATCAGCCCTGTCGCCACCTGGCTTCAAGAGAGCAGACACTTA
GAGGCTGGCGGGAAATGGGGAGGTGCGCCCTGGGAGGGCAGGCAGGGTTCCAAGGCCGTTCCCGTCCCTGGCG
CTGGAGTGACACAGCCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTAGATCACTGGTCCCCACCT
AGAAGGGTCCCCGCCCTAGATCAATCAGTGGACACTAAGGCACGTTAGAGTCTTGTCTTAATGATTATGT
CCATCCGTCTGTCCGTCCATTGTGTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACTTGTAGACTCGGTACAGTATCAAATAAA
ATCTATAACAGAAAAAA

FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNNNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDVTVDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRALHIKFTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAAGCTGGCACTGCGCGCTCTCCGT
CCCGCGGTGGTTGCTGCTGCCGTGCTGGGCCTGAACGCAGGAGCTGTCAATTGACT
GGCCCACAGAGGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACCTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT
GTGGATAATCCCGTGGGCACTGGGTTCAAGACATGATGGTTCTCCTGAAGACCTTCTCAGTTGCCACAAAG
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCAACTTGCGGGGGT
TGCCTTGGGTGATTCCCTGGATCTCCCTGGATTCTGGCTCTCCTGGGACCTTACCTGT
ACAGCATGTCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTGTCTTGTCAAGC
CACGTGAGACACCTACAACGAGATGCCCTAACGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTCCCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGTCAGGAGGCCTG
GGTGGAAAAGTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAGGCCCTGT
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTACTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTTCTTAAAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLP~~LLL~~GLNAGAVIDWPTEEGKEWVDYVTVRKDAYMF~~WW~~LYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
G~~T~~IKCNFAGVALGDSWISPVD~~S~~VLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAV~~N~~KGLYRE
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTM~~ESS~~LEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKII~~P~~DQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETS~~A~~FVKS~~Y~~KNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCAGGCCGTTATCAGGACCATGCAGGCCGA
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGACGCCGAACCTGGCGTTGGCGTGGCA
GGGGAGCCTGCGCCTGTGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGCGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGTCACCTGTCACCTACACTAAACACATCCAGCCCCTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCAGTGCACATCTCCCCACACCCTCCAGGAAGTTCAGGTGCCATCATAACA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAACGGCGGAAGGATGCCTGCTTCGGTACTCAGGTGGACCCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTCTACACCAATATCAGCCACCACCTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTGTCTTGTCTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAAGGCATTCTTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEELGRWPWQGSLRLW
DSHVCGVSLLSHRWALTAACFETYSSDLSDPSGMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWTGYIKEDEALP
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCGRPNRPGVYTNISHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCCACGCGTCCGGACGCGTGGGAAGGGCAGAATGGACTCCAAGCCTGCCTCCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCGGAGCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGTCCTGGCCGTGCGGACCCCTGAGGAAGAGAGCTGAGTCTCACCTT
GCCCTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGTGAGGCTGTGTCGGATCCCAG
CTCTCCTCAATAACGAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCCCTCCACACGGTGCAAAATGGCTCTTGGCAGCCGGAGGCCAGAAGTGCCATTCT
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCTTGGCCCCCATGTGGACTTTGTGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGCAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCTCTGTGATCCGTAAGCGATAACAACCTGACCTACAAGACGTGG
GCTCTGGCACCAGCAAACAGCCAAGCCTGTGCCAGTTCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTCATGCGCCTCTCGGTGGCAACTTGACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGGCGGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGCTGGTGCACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTCCTGCACTGGCTCATGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCGCTCGGGTCTCACCTGCTCTCGCCTCAGGTGACAGT
GGGGCCGGGTGTTGGTCTGTCTGGAAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAG
CCCCTATGTCACCACAGTGGGAGGCACATCCTCCAGGAACCTTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCCACGGCCTCATACCAGGAG
GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCCACCTGCCACCATCCAGTTACTTCATGC
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACTTCTGATGGCTACTGGTGGTCAGCAACA
GAGTGCCATTCCATGGGTGTCGGAACCTCGGCCTCTACTCCAGTGTGTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCCCCCCTCTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGGCAGGTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCCTGGCTGGATCCTGTAACAGGC
TGGGAACACCAACTTCCAGCTTGCTTGAAGACTCTACTCAACCCCTGACCCCTTCTATC
AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTCACTCCATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTATCTCCCTAACCCCTGAAA
TGCTGTGAGCTTGACTTGAATCCCACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCTTAGATTCTCAATAAGATGCTGTAACTAGCATTGTAATGCCTCTCCCTCCGC
ATCTCATCTTCTCTTCAATCAGGCTTCCAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCAATTCCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT
TTCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTGCTTATG
GCCTTCCATCATAGTTGCCACTCCCTCTCCTACTTAGCTTCCAGGTCTTAACCTCTCTG
ACTACTCTGTCTCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTG
TCCATTGAGATTTGCTTCTCAGTTACTCATTGCCCCGGAAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEPFLQWLM
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGCGCGCGCTCTCTCCGGGCCACACCTGTCTGAGCGGCGAGCGAGCCGGCCGGC
GGGCTGCTCGCGCGAACAGTGCTCGCATGGCAGGGATTCCAGGGCTCCTCTTCTC
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTG
GCCTGCATACCGCCTCCCTGCGTCTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCCAGTGTATAAGGAAACT
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTATGAAACGCTATGCCAATGG
CAGCCGACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAAAGGACTTCCTGCTCAACTACCCCTTCTAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCCCTGGTGGCAGAGAACGCATGTCCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAACGCTTCAGCCATGCCGAGCAGATGAA
AAGTTAAAGATGGTGGTCGAGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA
ATTTCAGTGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACTCAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGCCCTCTGCTAAGCAGCTGCCAGGGCCAGCGGGTCTGGGTCTAT
TGGTTATGACAATGACCGACCAGGCAATTGGTGTATCGCTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCTCTACCAGCAATGCGATGCCAGCCAGGGCCAGCGGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACGAGCGAAAAATTATTGGCATTTCAGG
GCACCAGTGGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAGAACACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG
TGACACAGTGTCCCTCTGGCAGCAATTAGGGCTTCATGTTCTTATTAGGAGAGGCC
AAATTGTTTGTCTTGCATTGGCGTGACACGTGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAATG
GTTTGTGTATCATATCATATCATTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAATGATTGGGCAATGAGGAATATTGACAATTAGTTAATCTCACGTTTG
CAAACTTGATTTCATCTGAACTTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAA

FIGURE 96

MAGIPGLLFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVL
TAACIHDGKTYVK
TQKLRVGFLLPKFKDGGRGANDSTS
SAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYD
YALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNL
VYRFCDVKDETYD
QQCDAQPGASGSGVYV
RMWKRQQQKWERKIIGIFSGHQ
WVDMNGSPQDFN
AVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTT
CTGGAGCGCCCCAGCCTGGGTGGGGCTGTCTCGGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCAGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCAGGGTTGTGGCGGGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACACTGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCACCTGTTCTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCTGGCTCTGGTCCCAGAAGGTGGTGTGCCTGGTGGAGC
CCCACCTGTGTATTCTGGAAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGCCTGCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCCTCAGACCCCTGCAGAAGCTGAAGGTTCTATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTGCGCACCGCTCTGGTGGAGAAGATCGTCAAGGGTGCA
GCTCCCGGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCC
CCCGCGCTCCTAGGGCGCAGCGGGACGCAGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTCGGGCGGCCTCGGCGGTTCCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGCCGGACGGCTGCTGCGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCTCCAAGGCATCAGGCCGCCAACGGCCTCATGTCCCCGCCAC
GACTTCCGGCCCCGCCCCGGCCAGCGCTTTGTGTATATAATGTTAATGATTGATT
AGGTATTGTAACCCTGCCACATATCTTATTATTCTCCAATTCAATAATTATTATT
CTCCAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLF SVLLGAWQLGNPGSRSQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHR SWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTGATGCTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGGGGCCAC
AACAAAGGAGCGCGGGCGCCGGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGGCCCTACCAGGAGGGACTC
CGTGCTCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCCTTACCTGGTAAC TGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTCCCTAGCAACGGGATTCCGGTTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGGAAACCCAGGCC
CCAACCTCCTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTCCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGCAAG
GGAACCTCCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTGCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGCTTGCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGGCCCTGGTCATGTGTGGGGCCCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGATCTTCTGAATGGGATACCACTCAAAGGG
TGAAGAGGTAGCTGTCCCTGTCACTTCCCCACCCCTGTCCCCAGGCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGCATGTGCCTCATCACACCCTCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCTCCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTT
TTTGAGTGGGGAGGCAGGGACGGAGGAAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFIMLLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPyQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMGTPLLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSMDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPPLLGLLLPPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTGAAAGTCAGGCTTCATTGGGAAGCCCCCTAACAGAACATTGGTCATTCTCCAAGTTATGGTGGACGT
ACTTCTGTTCTCCCTGCTTACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTCAT
CAAGGCAAGTTCCATGAGCACCTCAAAGCCTCGAGAAGTGAACAAACAAATGAATTGGAGACCATTCC
AAATCTGGGACCAGTCTCGCAAATATTACACTTCTCCTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
ACATCTGAAAGAGTTTCAGTCCCTGAAACTTGGACCTTAGCAGCAACAATATTCAGAGCTCAAACGTCATT
TCCAGCCCTACAGCTCAAATATCTGTATCTAACAGCAACCGAGTCACATCAATGGAACCTGGTATTTGACAA
TTTGGCCAACACACTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAAGATGTTAAACT
GCCCAACTGCAACATCTCGAATTGAACCGAAACAAGATTAAGGAGTAACTTATGGATGGAGCTTTGGGGCTGAGCAA
TGCTCTGAAAGTCTGAAAATGCAAAGAAATGGAGTAACTGAAACTTATGGATGGAGCTTACGGCTTGATGCT
GCAGGAACCTCATCTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTGCCAGAAGCTCAG
TGAGCTGGACCTAACCTCAACTTCAAGGTTAGATGATTCAAGCTTCCCTGGCTAAAGCTTAACTAAATAC
ACTGCACATTGGGAAACACAGACTCAGCTACATTGCTGATTGTGCCCTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAAGAACAAATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTGGGCTTGACAAACTGAG
GCGACTGATACTCCAAGGAAATCGGATCCGGTCTATTACTAAAAAGCCTCACTGGTTGGATGCATTGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGCTTACAAGGCAATGCATTCAACAAATGAAGAAACTGCAACAAATT
GCATTAAATACATCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCCACAGTGGTGGCGAAAACAACCTT
TCAGAGCTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAAGGAAGAAGCATTGGCTGTTAGCCCAGA
TGGCTTGTGTGATGATTCCCAAACCCAGATCACGGTTCAGCCAGAAACACAGTCGCGCAATAAGGTT
CAATTGAGTTCATCTGCTCAGTGCAGCAGCAGTGATTCCCAATGACTTTGCTGGAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAAATTATGCACACCTCCGGCCAAAGGTGGCGAGGTGATGGAGTATACCAC
CATCCTCGGCTGCGCAGGGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAATCACTTGGTT
ATCCTACTCTGCTAACAGCTAACAGTAAATATGCTTCCCTCATTCAACAGACCCCATGGATCTCACCAT
CCGAGCTGGGCCATGGCACGCTGGAGTGTGCTGTGGGGCACCCAGCCCCCAGATAGCCCTGGCAGAAGGA
TGGGGGCACAGACTCCCAGCTGCACGGAGAGACGCATGATGATGCCAGGATGACGTGTTCTTATCGT
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTGCAAATGC
AACTCTGACTGCTTAGAAACACCATCATTGGCCACTGTTGGACCGAAGTGTAAACCAAGGGAGAAACAGC
CGTCCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACGGACAAAGATGATAGCCATTGGTGG
AACCGAGAGGCACTTTGAGCAGGCAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGAA
ATACACATGTGAGATGTCTAACACCCCTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAAC
CTGCGACTCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGCCACTGTGGGTGTCGTGATCATAGC
CGTGGTTGCTGTGGTGGGCACGTCACTCGTGTGGTGGCATCATATAACCACACAAGGGAGGAATGAAGA
TTGCAGCATTACCAACACAGATGAGACCAACTGCCAGCAGATATTCTAGTTATTGTCATCTCAGGAAACGTT
AGCTGACAGGCAGGATGGGTACGTGCTTCAGAAAGTGGAAAGCCACCAAGGTTGTCACATCTCAGGTGCTGG
ATTTTCTTACCAACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAAAGCTGC
CACAGATCTGTCCTTGTCCCTGGATCCACAGGCCATTGTATTGAAGGGAAATGTGTATGGCTCAGA
TCCTTTGAAACATATCATAAGGTTGCAGTCCTGACCCAAGAACAGTTAATGGACCACTATGAGCCAGTTA
CATAAAGAAAAGGAGTGCTACCCATGTTCTCATCCTCAGAAGAACCTGCGAACGGAGCTCAGTAATATATC
GTGCCCTCACATGTGAGGAAGCTAACACTAGTTACTCTCACAAATGAAGGACCTGGAAATGAAAAATCTGTG
TCTAAACAAGTCCTCTTAGATTAGTGCACATTCCAGAGCCAGCAGCTGGTCTGGCTCGAGTAATTCTTCATGGG
TACCTTGAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTGGACAGCCATCAGATTGTCA
AAGAGCCTTTATTGAAAGCTATTCTCCCCAGACTGGACTCTGGGTAGAGGAAGATGGAAAGAAAGGAC
AGATTTAGGAAGAAAATCACATTGTACCTTAAACAGACTTTAGAAAACAGACTCCAAATTTCAGTC
TTATGACTGGACACATAGACTGAATGAGACCAAGGAAAGCTAACATACTACCTCAAGTGAACCTTATT
AAAGAGAGAGAATCTTATGTTAAATGGAGTTATGAATTAAAGATAAAATGCTTATTATACAGAT
GAACAAAATTACAAAAGTTATGAAAATTTTATACTGGGAATGATGCTCATATAAGAATACCTTTAAACTA
TTTTTAACCTTGTTATGCAAAAAGTATCTTACGTAATTAAATGATATAAATCATGATTATTTATGTATT
TTATAATGCCAGATTCTCATTATTTGCACATTATTTAATAAAATGTGTCAATTGAA
TTAAATAGAAGTTACTTCATTATTTGCACATTATTTAATAAAATGTGTCAATTGAA

FIGURE 102

MVDVLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQLSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRI SAI PPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE
FCQKLSELDLTFNHLSDLSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDDLKNNE
ISWTIEDMNGAFSGLDKLRRRILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWLPOWVAENNQSFVNASCAPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTER
HFFAAGNQLLIVDSDVSDAGKYTCMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLEDDG
WATVGVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLAD
RQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYVGSDPFETYHTGCPDPRTVLMHYEPSYIKKECYPCHPSEESCERSFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGTTGGTGCCTGCAAAATG
AAGGATGCAGGACGCAGCTTCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTTAGACCCGGGGGGTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTCCTCC
CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCAAAAGAAAAAGTATGTTCATTTCTC
TATAAAGGAGAAAGTGAAGCCAAGGAGATATTTGGAATGAAAAGTTGGGCTTTTAGTAAAGTAAAGAACT
GGTGTGGTGGTGTTCCTTCTTTGAATTCCCACAAGAGGAGAGGAAATTAAATAATACATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTTGACCGCGCAGATTGAGGCATTGATTGGGGAGAGGAAACCAGCAGAGCACAGTTGGA
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAAGTGGATTTCATCAACCTCCTTTTAAAT
TTTATTCCCTTGATCAAGATCATGCGTTCTCTGTCTTAACCACCTGGATTCCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACACTGTTGAATTCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCCCTGCTGTGGTGC
GCTGGCTCTCAACTTCTGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTCTGTGTGCTCTGCAGCAA
CCAGTTCAAGGTGATTGTGTTGGAAAAACCTGCGTGGAGGTTCCGGATGGCATCTCCACCAACACACGGCT
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCACTTGAGGCACCTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACATTGAAATTGGGCTTCATGGCTGGGAACCTCAACACTCTGGA
ACTCTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTGTATACTTGTCTAAACTGAAGGAGCTCTGGTT
GCGAAACAACCCATTGAAAGCATCCCTCTTATGCTTTAACAGAATTCCCTCTTGCGCCGACTAGACTTAGG
GGAATTGAAAAGACTTACATCATCTCAGAACGGTGCCTTGAGGTCTGCAACTTGAGGTATTGAACCTTGC
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAATAGATGAGCTGGATCTTCTGGAAATCA
TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTCCTCAAAACTGTGGATGATACAGTCCAGAT
TCAAGTGATTGAACGGAATGCCATTGACAACCTTCAGTCAGTAGTGGAGATCAACCTGGCACACAATAATCTAAC
ATTACTGCCTCATGACCTCTCACTCCCTGCATCATCTAGAGCGGATACATTACATCACAAACCTTGGAACTG
TAACGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCCCTGAACACAGCTGTTGTGCCGGTG
TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTGACCAAGAATTACTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCTGAGCTGAAATGTGGGCTCCACATC
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGCAGTAGCTGT
GCTCAGTGATGGTACGTTAAATTCAAAATGTAACGTGCAAGATAACAGGCATGTACACATGTATGGTGAGTAA
TTCCGTTGGGAATACTACTGCTTCAGCCACCTGAATGTTACTGCAGCAACCAACTCCTTCTTACTTT
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCACTCC
AGTGGTCGACTGGGAGACCACCAATGTGACCACCTCTCACACCAACAGCACAAGGTGACAGAGAAAACCTT
CACCATCCCAGTGACTGATATAAACAGTGGATCCCAGGAATTGATGAGGTATGAAGACTACAAAATCATCAT
TGGGTGTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTCTACAAGATGAGGAAGCAGCACCA
TCGGAAAAACCATCACGCCAACAAAGGACTGTTGAAATTATTAATGTGGATGAGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT
CAACACACAAACAGTTAACACAATAAATTCAATACACAGTTCACTGCAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAAAACAAACATCAAAAAAAA
GACAGTTATTAAAAATGACACAAATGACTGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAATTATTAAATTCTATTGTGATCTAAAGCAGACAAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWCNCDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVSNSVGN
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAAGTTGGCAGTTCTTCCGTTCCCTGCTGTTGGGGCA
TGAAAGGGCTTCGCCGCCGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCAGCGACCGC
GAGGGCGGGCGTGCACCCCTCGGCTGGAAGTTGTGCCGGGCCCCGAGCGCGCCGGCTGGGAGCTCGGGTAGA
GACCTAGGCCGCTGGACCGCGATGAGCGCGCCGAGCCTCCGTGCGCGCCGGGGTTGGGGCTGCTGCTGTGC
GCGGTGCTGGGCGCGTGGCCGGTCCGACAGCGGGCGTGCAGGGAACTCGGGCAGCCCTCTGGGGTAGCCGCC
GAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGACCTGACTGCAGTCAGTAAGCGGCTAGCGCTCTT
CCCGAGCCACTCCCCTGGTCCGCTCGGCTGGACTTAAGTCACAACAGATTATTCATCAAGGCAAGTTCC
ATGAGCCACCTTCAAAGCCTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCAGGAAATCTGGGACCA
GTCTGGCAAATATTACACTCTCCTTGGCTGGAACAGGGATTGAAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTGAAACTTGGACCTTAGCAGCAACAATATTCAAGGCTCCAAACTGCATTCCAGGCCACAG
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTTTTGACAATTGGCCAACACA
CTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTAAACTGCCCAACTGCAA
CATCTCGAATTGAAACGAAACAAGATTAAAAATGTAGATGGAACATTCAAGGCTTGGCTGCTGAAGTCT
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAACATGGAAATTG
CAGCTGGACCATAACAACCTAACAGAGATTACCAAGGCTGGCTTACGGCTGATGCTGCAGGAACCTCAT
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
ACTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCCTGGCTAACGTTACTAAATACACTGCACATTGGG
AACAAACAGAGTCAGCTACATTGCTGATTGCTTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAGAAC
AATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTGGGTTGACAAACTGAGGCGACTGATAACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCATTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGTCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAATTGCATTAAATACA
TCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGTGGCGAAACAAACTTCAGAGCTTGT
AATGCCAGTTGTGCCATCCTCAGCTGCTAAAGGAAGAACGATTGGCTTAGCCAGATGGCTTGT
GATGATTTCCAAACCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAGGTTCCAATTGAGTT
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTGCTGGAAAAAGACAATGAACACTGCATGAT
GCTGAAATGAAAATTATGCACACCTCCGGGCCAAGGTGGCGAGGTGATGGAGTATACCACCATCCTCGGCTG
CGCGAGGTGGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAATCACTTGGTCATCCTACTCTGTC
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCCATGGATCTCACCATCGAGCTGGGCC
ATGGCACGCTTGGAGTGTGCTGCTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGCCACAGAC
TTCCAGCTGCACGGAGAGACGCATGCATGTGATGCCAGGATGACGTGTTCTTATCGTGGATGTGAAGATA
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTCAGCAAATGCAACTCTGACTGTC
CTAGAAACACCATCATTGGCGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGCTTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAAACTGGACAAAGATGATAGCCCATTGGTGGTAACCGAGAGGCAC
TTTTGAGCAGGAAATCAGCTCTGATTATTGAGCTCAGATGTCAGTGCTGGAAATACACATGTGAG
ATGCTAACACCCCTGGCACTGAGAGAGGAAACGTGCGCTCAGTGTGATCCCCACTCCAACCTGCACTCCCT
CAGATGACAGCCCCATCGTAGACGATGACGGATGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTGCTGT
GTGGTGGGCACGTCACTCGTGTGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGATTGCAAGCATTACC
AACACAGATGAGACCAACTTGCAGCAGATATTCTAGTTATTGTCATCTCAGGAAACGTTAGCTGACAGGCAG
GATGGTACGTGCTTCAGAAAGTGAAGCCACCAAGTTGTCACATCTCAGGTGCTGGATTTTCTTACCA
CAACATGACAGTAGTGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGGAAGCTGCCACAGATCTGTT
CTTGTCCGTTTGGATCCACAGGCCATTGTATTGAAGGGAAATGTGTATGGCTCAGATCCTTGTAAACAA
TATCATACAGGTTGCACTGACCCAGAACAGTTAATGGACCACTATGAGCCAGTTACATAAGAAAAAG
GAGTGTACCCATGTTCTCATCCTCAGAAGAACGTTCTGCAACGGAGCTTCAGTAATATATCGTGGCCTTCACAT
GTGAGGAAGCTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAATCTGTGCTAAACAAGTCC
TCTTAGATTAGTGCACCCAGAGCCAGCGTCGGTGCCTCGAGTAATTCTTATGGTACCTTGGAAAA
GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAGCCAAGAGCCTTTAT
TTGAAAGCTCATTCTCCCCAGACTGGACTCTGGTCAGAGGAAGATGGAAAGAAAGGACAGATTTCAGGAA
GAAAATCACATTGTACCTTAAACAGACTTAGAAAACACAGGACTCCAAATTTCAGTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAGGAAAGCTTAACACTACCTCAAGTGAACCTTTATTAAAAGAGAGAGAAT
CTTATGTTTAAATGGAGTTATGAATTAAAAGATAAAAGCTTATTATACAGATGAACCAAAATTAC
AAAAGTTATGAAAATTAACTGGGAATGATGCTCATATAAGAATACCTTTAAACTATTTTAACTTTG
TTTATGCAAAAGTATCTACGTAATTAAATGATATAATCATGATTATTGATTGTTATAATGCCAGA
TTTCTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCATTTTAAATAGAAGTT
ACTTCATTATATTGCACTTAAATAAAAGTGTCAATTGAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAERPCPTTCRCLGDLLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRISSAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMGAFFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIRISPDAWEFC
QKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLSDLKNNEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRSIKKAAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQQLHLNTSSLLCDCQLKWLPOWVAEENNQSFVNASCAPQLLKGRSIFAVSPDGFVCDDF
PKPQITVQPETQSAIKGSNLNFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQGGE
VMEYTTIILRLREVEFASEGKYQCVISNHFGSSYVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRTVKGETAVLQCIAGGSPPPKNWTKDDSPQMTAPSLEDDGWA
FAAGNQLLIIVDSDVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLEDDGWA
TVGVVIIAVVCCVVGTSLVWVIIYHTRRNEDCSITNTDETNLPADIPSYLSSQGTLDLQ
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVYGSDFETYHTGCSPDPRTVLMMDHYEPSYIKKKECYPCHSEESCERSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAACCTGCGTCGCGGAGAGCGCCAGCTGACTTGAATGGAAGGAGCCGAGCCCGGGAGCGCAGCTGAGAC
TGGGGAGCGCGTTCGGCCTGTGGCGCCCTGGCGCCGGCGAGCAGGGAGGGCTATGGTGGTCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGGCCCTGGTGGTCCCTATCCCTCCTTATATA
GAAACCTCCACACTGGAAAGGCAGCGCGAGGCAGGGCTATGGTGGAGCAAGGAGGCCGCTGATCTGCAG
GCGCACAGCATTCCGAGTTACAGATTTACAGATACCAATGGAAGGCAGGAGGCAGAACAGCCTGCCTGGT
TCCATCAGCCCTGGCGCCAGGCAGTCAGCTGGCACCCCTGCAGGCACCATGGCCAGAGCCGGTGTGC
TGCTCCTGCTGCTGCCACAGCTGCACCTGGACCTGTGCTGCCGTAGGGCCAGGATTGGCCGAA
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTGCGGAGGAGGAGCCGGTGTGGTACTGAGCCCTGAGG
AGCCCGGGCTGGCCAGCCGGTCAGCTGCCCGAGACTGTGCCCTGTCAGGAGGGCGTGGACTGTG
GCGGTATTGACCTGCGTGAGTTCCCGGGGACCTGCCTGAGCACACCAACCTATCTCTGCAGAACACCAGC
TGGAAAAGATCTACCCCTGAGGAGCTCTCCCGCTGCACCGGCTGGAGACACTGAACCTGCAAAACACCAGC
CTTCCGAGGGCTCCCAGAGAACGGCTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC
TGACCTTGGCACCCCGCTTCTGCCAACGCCCTGATCAGTGTGGACTTGCTGCCAACTATCTCACCAAGATCT
ATGGGCTCACCTTGGCCAGAACCAAACCTGAGGTCTGTGTACCTGCACAACAAGCTGGCAGACGCCGGC
TGCCGGACAACATGTTAACGGCTCCAGCAACGTCGAGGTCTCATCCTGTCCAGCAACTTCTGCGCCACGTGC
CCAAGCACCTGCCCTGTACAAGCTGCACCTCAAGAACAAAGCTGGAGAACAGATCCCCCGGGCCT
TCAGCGAGCTGAGCAGCCTGCCGAGCTATAACCTGCAGAACAAACTACCTGACTGACGAGGGCTGGACAACGAGA
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTGGTCCAGCTGGGCTGC
CGCGCAGCCTGGTGTGCTGCACCTGGAGAACACGCCATCCGAGCGTGGACGCGAATGTGCTGACCCCATCC
GCAGCCTGGAGTACCTGCTGTCACAGCAACCAGCTGAGGCTTGGACAGGAGGAGGAGGAGGAGGAGG
TCAAGCGTTGCACACGGTGCACCTGTACAACAAACCGCCTGGAGAACACGCCATCCGAGCGTGGACGCGCTGG
GCACCCCTCATGATCCTGCACAACCAGATCACAGGCAATTGGCCCGAAGACTTGCCACCACCTACTTCTGGAGG
AGCTAACCTCAGCTACAACCGCATCACAGCCCACAGGTGCACCGCCTGGCAAGCTGCGCTGCTGC
GCTCGCTGGACCTGTCGGCAACCGGCTGCACACGCTGCCACCTGGCTGCCTCGAAATGTCCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCCTTGGCACGAGGGCGCTGGGGCATGGCTCAGCTGCGTGAAGCTGTACCTCA
CCAGCAACCAGCTGCCAGCCCTGGGCCCCGTGCCTGGTGGACCTCGCCATCTGCAGCTGCTGGACA
TCGCCGGAAATCAGCTCACAGAGATCCCCGAGGGCTCCCCGAGTCACCTGAGTACCTGTACCTGCAGAACAA
AGATTAGTGCAGGTCGGCCCAATGCCCTGACTCCACGCCAACCTCAAGGGATTTCTCAGGTTAACAAAGC
TGGCTGTGGCTCCGTGGTGGACAGTCCTCCGGAGGCTGAAGCACCTGCAGGTCTGGACATTGAAGGAA
TAGAGTTGGTGCACATTCCAAGGACCGTGGCCGCTGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAACAAGATAGTGCAGAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGACTTTCTGC
AGCACACGCCCTGTGTGAGCCCCCAGCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA
TCCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTCCAGGGCTGCCCACGCCAGACACATGC
ACACACATCACACCCCTCAAACACCCAGCTGCCACACACAACCTACCCCTCCAAACCACACAGTCTGTACAC
CCCCACTACCGCTGCCACGCCCTGTGAATCATGCAGGGAGGGCTGCCACACACACATGCACAAAGTCATGTGCGAA
TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACCACACACACATGCACAAAGTCATGTGCGAA
CAGCCCTCCAAAGCTATGCCACAGACAGCTCTGCCAGGCCAGAATGCCATAGCAGCTGCCGTGCGCC
GTCCCATCTGTCGTCCGTTCCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCACGCC
GGAACCTACAAAAGCTGGTTTATTCCCTTCCATCCATGGGGACAGGAGGCTTCAGGACTGCTGGCCTGGCC
TGGCCCACCCCTGCTCCTCCAGGTGCTGGCAGTCACCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACCTTCCAATGGCAAGCCAGTGGAGGCAGGATGGAGAGGCCCTGGGTGTGCTGGGGCCTGGGG
CAGGAGTGAAGCAGAGGTGATGGGGCTGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGAACAC
GTTCTCAGGCCTGTGGGGAAAGTCCGGTGCCTTATTCTTATTCTTAAGGAAAAAAATGATAAA
CTCAAAGCTGATTTCTTGTATAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLA
VAPGFGRSGGHSLSPPEENFAEEEPVLVLSPEEPGP
GPAVSCP
RDAC
SQEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEK
IYPEEL
SRLH
RLET
LN
LQNNR
LTSR
GLPE
KAFE
H
LT
LN
LYL
ANNK
LT
LAPR
FLP
NAL
ISV
DFA
ANY
LTK
IYGL
TFG
QK
PNL
RSV
Y
LH
NN
KL
ADAG
LP
DN
MFNG
SSNV
EV
LIL
SSN
FLR
HVP
KHL
PPAL
YKL
HL
KNN
KLE
K
IPPG
AF
SEL
SSL
RELY
LQNN
LT
DEGL
DN
ETFW
KLSS
LEY
LDL
SSNN
LSRV
PAGL
PRSL
VLL
H
LEK
NAIR
SVD
AN
V
L
TPI
RSLEY
LLL
HSN
QL
REQ
GIH
PLAF
QGL
KRL
HTV
HLYNN
ALER
VPS
GLP
RRV
RTLM
I
LHN
QIT
GIG
RED
FATTY
F
LEEL
NLS
YNR
ITS
PQV
HRD
AFR
KL
RL
RS
LDL
SGN
RL
HTL
PP
GLP
RN
V
HVL
KV
KR
NE
A
A
RG
ALAG
MA
QL
RELY
L
TSN
RL
RS
RAL
G
PRA
V
D
LA
H
L
QL
L
D
I
AGN
QL
TE
I
P
E
G
L
P
E
S
LEY
LYL
QNN
K
IS
AVP
AN
AFD
ST
PNL
KG
I
FLR
FN
K
L
AVG
SV
V
DSA
F
R
RL
K
HL
Q
V
LD
IE
GN
L
E
FG
D
IS
KD
RG
RLG
KE
KE
KE
KE
KE
KE
KE
TR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341, 477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493, 535-557

FIGURE 109

FIGURE 110

MDFLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGC DVVKGQIRCQCPSPGLHLAPDGRTCVDVDECATGRASCPRFRC
VNTFGSYICKCHKGFDLMLYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWI PDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTPERPTTGLTTIAPA AASTPPGGITVDN
RVQTDPQKPRGDVFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPA GGQYLTVSAAKAPGG
KAARLVLPLGRLMHSGLLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSEQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACCTTCCTTGCACAGGTGCTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTAGGCCCTACCTACCCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCCA
ACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGGAAATACC
AACACAAAGTTACCATGATGCCACCCAAATGCATCTGCTTATCAACCCACTGCAGTTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTAGGGAAATGGAACCTATGCCAGTCA
GAAGATAACAAGTCACGGTTGATGATCCTGTCACAAAGCCAGTGGTGCAGATTCATCCTCCCT
CTGGGGCTGTGGAGTATGTGGGAACATGACCTGACATGCCATGTGGAAGGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAATTACAGCT
GCCTGGTGAGGAACCCGTCAAGTGAATTCTGATAAAAGGGCTAAAGTAGGGAAAGTGTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAAGCATGGCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAAACATAAC
CGGCAGGCAAGATGAAACTCATTCACAGTTATCATCACTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAATCATTGTCACCTTAGCAAGTATAACTGGAATATCACTATTGATT
ATATCCATGTGTCTTCTCTTCTATGGAAAAAAATATCAACCCCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAACAGAACATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGTGTGTTCCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGATCGGGCAAGATTGCACAGTACAGT
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATTCAAGACTTGAACTTCTATGG
GCTAAACAGTACATTGAGTGAAAATTCTGAAGAACATTAAAGGAAAAACAGTGGAAAAGT
ATATTAATCTGGAATCACTGAAGAACACCAGGACCAACACCTCTTACTCATTATTCTTACA
TGCAGAACAGGGCATTATGCAAATTGAACCTGCAGGTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGAAATTCCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGGTTCTCATAAGTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTACATTGTTGATTTCAGCAGACTTGTGTTATTAAATTGTTATTAGTG
TTAAGAACGCTAAATTATGTTCAATTTCAGGAAATTCTATCTGTTATTGTACAA
CAAAGTAATAAGGATGGTGTCAACAAAACAAACTATGCCTCTTTTTCAATCACC
AGTAGTATTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA
TTTTTTCAAGGAAAGATGGATTCAAATAATTCTGTTGCTTTAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNVKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGCGAAATGGCGCCCTCCGGGAGTCTGCAGTCCCCTGGCAGTCCTGGTGTGTT
GCTTGGGGTGCTCCCTGGACGCACGGCGGAGCAACGTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTATGCCCCGTGGTCCCCTGCT
TGTCAAAAATCTTCAACCGGAATGGAAAGTTTGCTGAATGGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTATCATTGAAAGATGGTGAATTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAAACTTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGGCCGTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTATTGAAGACCTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCCTTGCCTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAAAAAAT
TATTATCAGAACATCTGCACAACCTTGAAAAAGTGGAGGAGGAACAAGAGGCCGATGAAGAA
GATGTTCAGAAGAACAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAACATGC
CATAAGAACACGCTCTGGTCCATCATTGCCACAGATAAATCCTAGTTAAATTATAG
TTATCTTAATATTATGATTGATAAAACAGAACGATTGATCATTGTTGGTTGAAGTG
AACTGTGACTTTTGAAATTGCAGGTTCACTAGTCTAGATTGTCATTAAATTGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTATAACAGTTGAAATATGATTAAAGCACAGTATGATG
GTTAAATAGTTCTCAATTGTTGAAAAATCGTCCAAGCAATAAGATTATGTATATTGT
TTAATAATAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAAGTATTGCATTAT
TGAGGTATTTAAGAACGATTATTAGAGAAAAATATTCTCATTGATATAATTCTCTG
TTCACTGTGTGAAAAAGAACGATATTCCATAAATGGGAAGTTGCCATTGTCTCAAG
AAATGTGTATTCACTGACAATTCTGGTCTTTAGAGGTATTCCAAAATTCCATTGT
ATTTTTAGGTTATGCAACTAAACACTACCTTACATTAAATTACAGTTCTACACA
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCACTGGTATTCTTGATTC
CAACAAAGTTGATTCTCTGTATTCTACTTACATTACAGTTCACTGGTACATTTTTATT
CAAATTGGATGATAATTCTTGAAACATTGTTATGTTAGTAAACAGTATTGTTGTT
GTTCAAACGTGAAAGTTACTGAGAGATCCATCAAATTGAACAACTGTTGTAATTAAAATT
TTGCCACTTTTCAGATTACATCATTCTGCTGAACATTCTGATTGTCATTGAAATTGTTTT
TTCTTTGGATGTGAAGGTGAACATTCTGATTGTCATTGTCATTGAAAGCCTGGTA
TTTACATTGAAATTCAAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAAG
CATCTTCTGTATATGTCTAAATGTATTGTCCTCATATAACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTGATTGTTAAAATAAACATTGTTATTTTAAAGACAA
ACTTCATATTATCCTGTGTTCTTCCCTGACTGGTAATTGTCGTTGGGATTCACAGGTAAA
GTCAGTAGGATGGAACATTAGTGTATTTCATTCTAAAGAGCTAGAACATAGTTT
CACCTTAAAGAACGGGGAAATCATAAAATACAATGAATCAACTGACCATTACGTAGTAGAC
AATTTCGTAAATGTCCTCTTCTAGGCTCTGTTGCTGTGAATCCATTAGATTACAG
TACCGTAATATAACAGTTCTTAAAGCCCTCTCCTTAAAGTAAATTAAATATTGTA
AAAGAGTTGGATGTGTAATTGTCATTGCTAGAAAAATATCCTAACGACAAAATAACCT
TTCTAACCACTTCATTAAAGCTGAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGPWTHGRRSNVRVITDENWRELLEGDWMIIFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCP SKRRPQPYPYPSKKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCAGTGTCCAGCTGCGGAGACCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG
AAGGTCTGGCCCAGAGCAGTGTGACACTTCCCTGTGACCATGAAACTCTGGGTGTCTGC
ATTGCTGATGGCCTGGTTGGTGTCTGAGCTGTGAGGCGAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGCAGTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGGCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGATGCTGAGGGCTACCTGGCTACCCCTGTGAATGCCTACAAACTGG
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGTGCA
GGTTTATGCCAACCTCTGTGAGCAGCTTCCCCACTGATGAGGACGAGATAGG
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGGAACCTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GGCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGTCTCCAGTTGGGTGATCTGCACCGTGCCTGGAGCTCACCCGCCCTGCTC
TCCCTGACCCAAGCCACGAACGAGCTGGAGGAAATCTGCGGTACTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAACGCTGAGCTAGCAACCCCAGAAGGCA
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTGTGCTGGG
GAGGGTGTCAAACGTACACCCCCGTAGACAGAACGAGGCTTCTGTAGGTACCCATGGCAA
CAGGGCCCCACAGCTGCTATTGCCCTCAAAGAGGAGGACGAGTGGGACAGCCCGACA
TCGTCAGGTACTACGATGTCATGTGATGAGGAAATCGAGAGGGATCAAGGAGATCGAAAAA
CCTAAACTTGCACGCCACCGTTGTGATCCAAAGACAGGAGTCCTCACTGTCGCCAGCTA
CCGGTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCCTGTTGTGGCCGAGTAAATC
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGAGGACAGTATGAACCGCACTCGACTTCTCTAGGCGACCTTGTACAGCGG
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG
GTGGTGCACCCTGATCTGGGCTGCAAGTGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTCT
TGAGACCTTGTGGATCAACAGAAGTTGACTTGACATCCTTCTGTCCCTCCCTGGTC
CTTCAGCCCAGTCAACGTGACAGACACCTTGTATGTTCTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCCAGCCCTCCATTAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCAAGTGAACCAAAAGTTCTGATACCTTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACCAAAAAATAAAATGTCCCTACCAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGEELPGTKYQAMLSVDDCFGMGRSAYNEGDDYHTV
LWMEQVLKQLDAGEEATTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEREKTLTNQTEAELATPEGIYERPVDPYLPERDVYESLCRGEVKLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMDSDEEIERIKEIAPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATFPDLGAAIWPKKGTAVFWYNLLRSGEDYR
TRHAAACPVLVGCKWVSNKFHERGQEFLRPCGSTEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTACTCCTCCTTTAGTGGAAAGACAGACATAATCCCAGTGTGAGTGAAATTGATTGT
TTCATTATTACCGTTGGCTGGGGTTAGTCCGACACCTCACAGTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTTCTGGGATGCTGGCCTGGAAGCCAGCAGGGCTTGCTCTGCTCTTGGCTCATTGACCC
CAGGTTCTCTGGTAAAAGCCTACTACTGGCCTGGCTCCATCAATCCATTGATCCTTGAGGCTGTGCC
CCTGGGCACCCACCTGGCAGGGCCTACCACCATGCACTGAGCTCCCTGTTGGCTCTGCTGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCTGGGTGCAGCCTGAGCCTGAGGGTTCTGGATCCAGGGGAGGGAGAAG
ATCCCTGTGTCGAGGCTGTAGGGAGCGAGGAGGGCACAGAATCCAGATTGAGAGCTCGCTAGACCAAAGTG
ATGAAGACTTCAAACCCGGATTGTCCCCTACTACAGGGACCCAAACAAGCCTACAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGCTCCCGTGAACGGTTGCTGGCTGACCTCCGAGCTACACTGTCCA
CTTGGCGTGGCTGTGAACCGTACGGTGGCCATCACTCCCTCGGTACTCTACTTCACGGCAGCGGGGG
CCCGGGCTCCAGCAGGATGCAAGGTGGTCTCATGGGATGAGCAGGCCCTGGCTCATGTCAGAGACCTGC
GCCACCTTCACACACACTTGGGGCGACTACGACTGGTCTTCATCATGCAAGGATGACACATATGTGCAAGGCC
CCCGCCTGGCAGCCCTGCTGGCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGCAGAGGAGTTATTG
GCGCAGGCGAGCAGGCCGTACTGTCACTGGGGCTTGGTACCTGTTGTCACGGAGTCTCTGCTCGTGC
GCCACATCTGGATGGCTGCCGAGGAGACATTCTCAGTGCCGTGACGAGTGGCTGGACGCTGCCATTG
ACTCTCTGGCGTCGGCTGTCTCACAGCACCAGGGCAGCAGTATCGCTCATTTGAACGGCAAAATAGGG
ACCTGAGAAGGAAGGGAGCTGGCTTCCCTGAGTGCCTCGCCGTGCACCGTCTCGAAGGTACCCCTCATGT
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGAGCAGGGCTTACAGTGAACATAGAACAACTGCAAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCCTTCA
CACCAACTCTGCTTGAGGTGCTGGCTGGACTACTTCACAGAGCAGCACACCTCTCCTGTCAGATGGGG
CTCCAAGTGCCACTACAGGGGCTAGCAGGGCGACGTGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGGCGCTATCAGCCCCGCCTGCGCTCCAGAACGAGCGACTGCTCAACGGCTATGGCGCTCGACCCAGCAC
GGGCATGGAGTACACCCCTGGACCTGCTGGAAATGTGTGACACAGCGTGGCACCGGCCCTGGCTCGCA
GGTCAGCCTGCTGGGCCACTGAGCCGGGGAAATCCTACCTATGCCCTATGTCAGGAGCAGCCACCGAGTGC
AGCTGGTGTGCCACTCCTGGTGGCTGAAGCTGCTGCAAGCCCCTGGCTTCCCTGAGGCCTTGAGCCAATGTCC
TGGAGCCACGAGAACATGCATTGCTCACCTGTTGCTGGCTACGGCCACGAGAAGGTGGCCGTGGAGCTCCAG
ACCCATTCTGGGGTGAAGGCTGCAGCAGGGAGTTAGAGCGACGGTACCCCTGGACGGCTGGCTCG
CTGTGCGAGCAGAGGCCCTCCCAGGTGCGACTCATGGACGTGGCTCGAAGAACGACCCCTGTGGACACTCT
TCTTCCATTACCAACCGTGTGGACAAGGCCCTGGCCGAAGTCTCAACCGCTGCGATGAATGCCATCTCTGGCT
GGCAGGCCCTCTTCCAGTCCATTCCAGGAGTTCAATCCTGCCCTGTCACCCACAGAGATACCCCCAGGGCCC
CGGGGCTGCCCTGACCCCCCTCCCCTGGTGGCTGACCCCTCCCAGGGGCTCTATAGGGGGAGATTG
ACCGGCAGGCTCTCGGGAGGGCTGCTTACAAACGCTGACTACCTGGCGGCCAGCCCGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGGCTGGAGGGTATGGATGTTTCCCTGGTCTCAGGGCTCC
ACCTCTTCCGGCCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAAGCCCACGGCTCAGTGAAG
AACTCTACCAACCGCTGCCGCTCAGCAACCTGGAGGGCTAGGGGGCGTGGCTATGGCTCTCTTGAAG
AGCAGGAGCAGGCCAATAGCACTTAGCCGCTGGGGCCCTAACCTCATTACCTTCTTGTCTGCCCTCAGCC
CCAGGAAGGGCAAGGAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTAAATATGAAAATGTTATTAA
ACATGTCTTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFYLLSRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMEYTL DLL ECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLPPLL
VAEAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLRCRMNAISGWQAFFP
VHFQEFNPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRQLAMALFEQEANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCACCGTGGAGAGGAAACCGTGCCTGGCTGCCTTCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTATGGAAATAGAA
TGCACCAACATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTGAAAATTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGGCTGCAGTAAGGAGACTGGACAAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTGATAAGTATAGAGACCAATACAAC
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTAATACAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC
CAACCAGGTAGTAGAAGGCTGTTAGATGCTGTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGTATGGGTATACCGCCTAGGGCATTTGGCATATTTCAAT
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTTGAGAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTGTTGTCATTATTGAGTACTACATATCCAA
TACAGCTGTATGTTCTTTCTTCTAAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTAAATGAGGGTGGTTCTTAAACACATGAACATTGAAATG
TGTTGGAAAGTGTGTTAAGAATAATAATTGCAAATAACTATTAAATAATTAT
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACCTTAGCTGTGTTCCCTTACTTCTAAACTGATTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTGCCTCTCAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSENVKFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAAGAGAGAGAGAGAAACAAAAACCAAAAGAGAGAGAAAAAATGAATTCACTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCAAATGTTCTATGGACTGTTGCT
GGGATCCCCATCCTATTCTCAGTGCCTGTTCATCACCAGATGTGTTGACATTCGCAT
CTTCAAAACCTGTGATGAGAAAAAGTTCAGCTACCTGAGAATTTCACAGAGCTCCTGCT
ACAATTATGGATCAGGTTCAGTCAAGAATTGTTGCCATTGAACGGAAATTTCATCC
AGCTGCTACTTCTTTCTACTGACACCATTCCCTGGCGTTAACGTTAAAGAAACTGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAAACTCACAGGAGGAGCAGGAATTCCCTTACAAGA
AACCTAAAATGAGAGAGAGTTTATTGGACTGTCAGACCAGGTTGTCAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGATGTAGGGAGGCCAACAA
CATAGCTACCCCTGGAGGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAAGGCAAAATTGGA
ATGATGTAACCTGTTCTCAATTATTCGGATTGTGAAATGGTAGGAATAAAATCCTTG
AACAAAGGAAAATCTCTTTAAGAACAGAACAGGACAAACTCAAATGTGTAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTGTGCGCTGAACCTCAAAGGACTTC
ATAAGTATTGTTACTCTGATACAAATAAAATAAGTAGTTAAATGTTAAAAA
AAAAA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCYNYGGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCCGCGCTGCCGCTGGCCCTCAGCAACCCTGACATGGCGCTGAGGCCACCGCGAC
TCCGGCTCTGCCTGGCTGCCTGACTTCTCCTGCTGCTGCTTTCAAGGGCTGCCTGATAAGGGCTGAAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTGCATCATTACGGATTGCG
AGACAAGTGAACCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGTCGTGCAGAAATACTGGGAAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCACTAGGCAAGGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT
CCAGAGCCAATCCCAGATTGCAATTCTCTTCCACTTAAACTCTGAAACAGGCACTTGGTGTCACTGCTG
TTCACAAGGACGACTCTGGGAGTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTCTGGTGTCTGACTGCCCTGA
TCACGTTGGCATCTGCTGTGCATAACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCAGTCAGACACAAGTCATCGTTG
TGATCTGAGACCCCGGGTGTGGCTGAGAGCCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTAGAAGCTTTCGTTGGCCAAAGTTGACCA
CTACTCTTACTCTAACAGCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAAATATAACCACAA
GGAAGCGAAACTGGGTGCGTTACTGAGTTGGTCTTAATCTGTTCTGGCCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTGCTCACGTAACAGCCCGTGTGGCCCTGTGAAGCCAGCATGTTACCACTGGTCGTT
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCGGCGGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTACTTCATCGGCCACAGACACCACCGCAGTTCTTAAAGGCTCTGC
TGATCGGTGTTGCACTGTCATTGTGGAGAAGCTTTGGATCAGCATTGTTAAACAAACCAAAATCAGGAAG
GTAAATTGGTTGCTGGAAGAGGGATTTGCTGAGGAACCTGCTTGTCCAACAGGGTGTAGGATTAAAGGAAA
ACCTCGTCTTAGGCTAACGACTGAAATGGTACTGAAATATGCTTTCTATGGGTCTTGTATTAAACATATTGT
TACATCTAAATTGGCTAACGATGTATTGATTATTGAAAGAAAATTCTATTAAACTGTAATATATTGT
CATACAATGTTAAATAACCTATTGGTAAAGGTTAAACAGGAACTCATACTGTCTACACATCAGACCATAGTGCTTAGGAAACCTT
TAAAATTCCAGTTAACGAAATCAGTTGCATCTCTCAAAAGAACCTCTCAGGTTAGCTTGA
GCCTCTCCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAACGCCCTCAGATGTACATACACAGATG
CCAGTCAGCTCCTGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTCCTCGCTGCTGCCAGGAGGCCCT
GCCATCCTGGGCCCTGGCAGTGGCTGTCCCAGTGAGCTTACTCACGTGGCCCTGCTCATCCAGCACAGC
TCTCAGGTGGGCACTGCAGGGACACTGGTCTTCCATGTAGCGTCCCAGCTTGGCTCCTGTAACAGACCTCT
TTTGGTTATGGATGGCTCACAAATAGGGCCCCAATGCTATTGTTAAAGTTGTTAATTATTGTT
AAGATTGTCTAACGGCAAAGCAATTGCAAAATCAAGTCTGTCAAGTACAATAACATTAAAGAAAATGGAT
CCCACGTCTCTTTGCCACAGAGAAAGCACCAGACGCCACAGGCTCTGCGATTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTAAAGAACGTCAAGGTGGAGCAGCCAGGTGAAAGGCTGGGGAGGAAAG
TGAAACGCCCTGAATCAAAGCAGTTCTAATTGACTTTAAATTTCATCCGCCGGAGACACTGCTCCCATT
TGTGGGGGACATTAGCAACATCACTCAGAACCTGTTCAAGAGCAGGTGTTCTCAGGCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCTGGA
GAATGGCTCTCACTCACCTGTTCAAGCTCCAGTGTCTGGTTTTTATACTTGTACAGCTTTTTT
AATTGCATACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGCAGGCCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGTCTCCCTGGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTTGGGATTCAAGCTCCAGCCTCCT
TCTTGGTTGTCATAGTGTAGGGTAGCCTTATTGCCCCCTTCTTACACCTAAACCTTACACTAGTGCCA
TGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTGGATGGATGGTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTATAAAAGCTTCAAAAAACCCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267